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OM protein - protein search, using sw model

Run on: March 15, 2004, 07:38:19 / Search time 53 Seconds
(without alignments)
581.088 Million cell updates/sec

Title: US-09-620-955b-4
Perfect score: 109
Sequence: 1 QSALTQPAVSAGSPGQSIIT.....CSSFANSGLPGGRTVTVL 109

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 916823

Minimum DB seq length: 0

Maximum DB seq length: 109

Post-processing: Listing first 100 summaries

Database : A_Geneseq_29Jan04:*

1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	109	100.0	109	4	AB069602 Huntingti
2	28	25.7	90	6	ABJ18698 Antibody
3	28	25.7	95	4	ABG12881 Novel hum
4	28	25.7	95	7	AD080993 Novel pro
5	26	23.9	104	2	AA038596 Human lam
6	26	23.9	104	2	AA038596 Human lam
7	23	21.1	27	6	ABP56815 Human lam
8	22	20.2	22	5	AAU70414 Human lig
9	22	20.2	94	2	AA022580 Light cha
10	22	20.2	100	3	AA01957 Wild-type
11	22	20.2	100	3	AA01957 Wild-type
12	21	19.3	92	3	AA01957 Wild-type
13	21	19.3	97	4	AB039374 Peptide #
14	21	19.3	97	4	AB039374 Peptide #
15	21	19.3	97	4	AB039374 Peptide #
16	21	19.3	97	4	AB039374 Peptide #
17	21	19.3	97	4	AB039374 Peptide #
18	21	19.3	97	4	AB039374 Peptide #
19	21	19.3	97	4	AB039374 Peptide #
20	21	19.3	97	4	AB039374 Peptide #
21	21	19.3	97	4	AB039374 Peptide #
22	21	19.3	97	4	AB039374 Peptide #
23	21	19.3	97	4	AB039374 Peptide #
24	21	19.3	97	4	AB039374 Peptide #
25	21	19.3	97	4	AB039374 Peptide #

26	17	15.6	104	6	AB027433 Anti-Rh(D
27	17	15.6	108	4	AB027432 Anti-Rh(D
28	17	15.6	108	4	AB027432 Anti-Rh(D
29	14	12.8	17	5	AA017909 T-cell re
30	12	11.0	90	4	AB048026 Light cha
31	12	11.0	97	5	AB043164 Human ova
32	12	11.0	99	3	AB040148 Anti-hl1
33	12	11.0	99	6	AB056516 Human ant
34	12	11.0	101	2	AA038604 NEW1 ligh
35	12	11.0	103	2	AA038605 NEW1 ligh
36	12	11.0	103	2	AA038605 NEW1 ligh
37	12	11.0	103	2	AA038605 NEW1 ligh
38	12	11.0	103	2	AA038605 NEW1 ligh
39	12	11.0	104	6	AA038605 NEW1 ligh
40	12	11.0	104	6	AA038605 NEW1 ligh
41	12	11.0	104	6	AA038605 NEW1 ligh
42	12	11.0	104	6	AA038605 NEW1 ligh
43	12	11.0	104	6	AA038605 NEW1 ligh
44	12	11.0	104	6	AA038605 NEW1 ligh
45	12	11.0	104	6	AA038605 NEW1 ligh
46	12	11.0	104	6	AA038605 NEW1 ligh
47	12	11.0	104	6	AA038605 NEW1 ligh
48	12	11.0	104	6	AA038605 NEW1 ligh
49	12	11.0	104	6	AA038605 NEW1 ligh
50	12	11.0	104	6	AA038605 NEW1 ligh
51	12	11.0	104	6	AA038605 NEW1 ligh
52	12	11.0	104	6	AA038605 NEW1 ligh
53	12	11.0	104	6	AA038605 NEW1 ligh
54	12	11.0	104	6	AA038605 NEW1 ligh
55	12	11.0	104	6	AA038605 NEW1 ligh
56	12	11.0	104	6	AA038605 NEW1 ligh
57	12	11.0	104	6	AA038605 NEW1 ligh
58	12	11.0	104	6	AA038605 NEW1 ligh
59	12	11.0	104	6	AA038605 NEW1 ligh
60	12	11.0	104	6	AA038605 NEW1 ligh
61	12	11.0	104	6	AA038605 NEW1 ligh
62	12	11.0	104	6	AA038605 NEW1 ligh
63	12	11.0	104	6	AA038605 NEW1 ligh
64	12	11.0	104	6	AA038605 NEW1 ligh
65	12	11.0	104	6	AA038605 NEW1 ligh
66	12	11.0	104	6	AA038605 NEW1 ligh
67	12	11.0	104	6	AA038605 NEW1 ligh
68	12	11.0	104	6	AA038605 NEW1 ligh
69	12	11.0	104	6	AA038605 NEW1 ligh
70	12	11.0	104	6	AA038605 NEW1 ligh
71	12	11.0	104	6	AA038605 NEW1 ligh
72	12	11.0	104	6	AA038605 NEW1 ligh
73	12	11.0	104	6	AA038605 NEW1 ligh
74	12	11.0	104	6	AA038605 NEW1 ligh
75	12	11.0	104	6	AA038605 NEW1 ligh
76	12	11.0	104	6	AA038605 NEW1 ligh
77	12	11.0	104	6	AA038605 NEW1 ligh
78	12	11.0	104	6	AA038605 NEW1 ligh
79	12	11.0	104	6	AA038605 NEW1 ligh
80	12	11.0	104	6	AA038605 NEW1 ligh
81	12	11.0	104	6	AA038605 NEW1 ligh
82	12	11.0	104	6	AA038605 NEW1 ligh
83	12	11.0	104	6	AA038605 NEW1 ligh
84	12	11.0	104	6	AA038605 NEW1 ligh
85	12	11.0	104	6	AA038605 NEW1 ligh
86	12	11.0	104	6	AA038605 NEW1 ligh
87	12	11.0	104	6	AA038605 NEW1 ligh
88	12	11.0	104	6	AA038605 NEW1 ligh
89	12	11.0	104	6	AA038605 NEW1 ligh
90	12	11.0	104	6	AA038605 NEW1 ligh
91	12	11.0	104	6	AA038605 NEW1 ligh
92	12	11.0	104	6	AA038605 NEW1 ligh
93	12	11.0	104	6	AA038605 NEW1 ligh
94	12	11.0	104	6	AA038605 NEW1 ligh
95	12	11.0	104	6	AA038605 NEW1 ligh
96	12	11.0	104	6	AA038605 NEW1 ligh
97	12	11.0	104	6	AA038605 NEW1 ligh
98	12	11.0	104	6	AA038605 NEW1 ligh

99 11 10.1 106 5 ABP66410
100 11 10.1 106 5 ABP66414

ABP66410 Human RSV
ABP66414 Human RSV

ALIGNMENTS

RESULT 1
AAB69602

ID AAB69602 standard; protein; 109 AA.

XX AAB69602;

DT 30-APR-2001 (first entry)

DE Huntingtin minimal sfv binding region #2.

XX Neurological disorder; Huntington's disease; Alzheimer's disease;

KM Parkinson's disease; prion disease; frontotemporal dementia;

KM amyotrophic lateral sclerosis; spinal and bulbar muscular atrophy;

KM dentatorubral-pallidoluysian atrophy; spinocerebellar ataxia type 1; SCA2;

XX SCA3; SCA4; SCA5; SCA6; SCA7; protein accumulation; intrabody.

XX Unidentified.

OS WO200106989-A2.

XX 01-FEB-2001.

XX 24-JUL-2000; 2000WO-US020131.

XX 27-JUL-1999; 99US-0146047P.

XX 21-JUL-2000; 2000US-00620955.

XX (HUST/) HUSTON J S.

XX (MESS/) MESSER A.

XX (LECE/) LECERF J.

XX Huston JS, Messer A, Lecerf J;

XX WPI; 2001-182700/18.

XX N-PSDB; AAF58706.

XX Inhibiting intracellular polypeptide accumulation, useful for treating

PT neurological disorders, e.g. Alzheimer's disease, comprises contacting

PT the polypeptide with a specific intrabody.

XX Claim 21; Page 94; 108pp; English.

XX The present invention describes a method for inhibiting the formation of

CC aggregates of certain proteins, involving contacting the protein with a

CC binding molecule known as an intrabody. Proteins to be bound include

CC those associated with neurological disorders, and so the method can be

CC used in the prevention of diseases such as Alzheimer's, Parkinson's and

CC Huntington's diseases, prion disease, frontotemporal dementia,

CC amyotrophic lateral sclerosis, spinal and bulbar muscular atrophy,

CC dentatorubral-pallidoluysian atrophy, spinocerebellar ataxia type 1

CC (SCA1), SCA2, SCA3, SCA4, SCA5, SCA6 and SCA7

XX Sequence 109 AA;

Query Match 100.0%; Score 109; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 2.6e-99;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSALTQPAVSGSPGQSIITISCTGTSDDIGAYVYVMYQYPGKAPKLLIYDVSNRPSGI 60
DB 1 QSALTQPAVSGSPGQSIITISCTGTSDDIGAYVYVMYQYPGKAPKLLIYDVSNRPSGI 60
QY 61 SNRPSGSKSGDTASLTISGLQAEADYYCSPFANSGLPFGGGTKYTVL 109
DB 61 SNRPSGSKSGDTASLTISGLQAEADYYCSPFANSGLPFGGGTKYTVL 109

RESULT 2
ABJ18698

ID ABJ18698 standard; protein; 90 AA.

XX ABJ18698;

DT 06-MAR-2003 (first entry)

DE Antibody library related human protein sequence SEQ ID No 27.

KM library; recombinant antibody; clustering variable region; in silico;

KM immunogenicity; antibody therapeutic; human.

XX Homo sapiens.

OS WO200284277-A1.

XX 24-OCT-2002.

XX 17-APR-2002; 2002WO-US012202.

XX 17-APR-2001; 2001US-0284407P.

XX (ABMA-) ABMAXIS INC.

XX Luo P;

XX WPI; 2003-093043/08.

XX Constructing a library of recombinant antibodies useful as source of

PT antibody candidates for screening antigens comprises clustering variable

PT regions of antibodies having known 3-dimensional structures into

PT structural ensembles.

XX Disclosure; Page 116; 119pp; English.

XX The invention relates to a novel method for the construction of a library

CC of recombinant antibodies. The novel method comprises clustering variable

CC regions of a collection of antibodies having known 3D structures into at

CC least two families of structural ensembles, each comprising at least two

CC different antibody sequences but with substantially identical main chain

CC conformations. The method is useful for constructing a library of

CC artificial antibodies in silico which provides a structurally diverse and

CC yet functionally more relevant source of antibody candidates which can

CC then be screened for binding a wide variety of target molecules,

CC including small molecules, and biomacromolecules such as proteins,

CC peptides and nucleic acids. The libraries constructed are useful as a

CC source of antibody candidates for further screening for novel antibodies

CC with high affinity against a wide range of antigens and having no or

CC minimum immunogenicity to human subjects treated with antibody

CC therapeutics. This sequence represents a human peptide region of an

CC antibody relating to the novel antibody library construction method of

CC the invention

Query Match 25.7%; Score 28; DB 6; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSALTQPAVSGSPGQSIITISCTGTSDD 28
DB 1 QSALTQPAVSGSPGQSIITISCTGTSDD 28
QY 13-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #12872.
 XX KM Human; chromosome mapping; gene mapping; gene therapy; forensic;
 XX KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX OS Homo sapiens.
 XX PN WO200175067-A2.
 XX PD 11-OCT-2001.
 XX PF 30-MAR-2001; 2001WO-US008631.
 XX PR 31-MAR-2000; 2000US-00540217.
 XX PR 23-AUG-2000; 2000US-00649167.
 XX PA (HYSE-) HYSEQ INC.
 XX PI Drmanac RT, Liu C, Tang YT;
 XX DR WPI; 2001-639362/73.
 XX DR N-PSDB; AAS77068.
 XX PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX PS Claim 20; SEQ ID NO 43240; 103bp; English.
 XX XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG0377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pot_sequences
 XX SQ Sequence 95 AA:
 QY Query Match 25.7%; Score 28; DB 4; Length 95;
 DB Best Local Similarity 100.0%; Pred. No. 1.4e-19;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 QSALTQPASVSGSPGSGITISCTGSSD 28
 24 QSALTQPASVSGSPGSGITISCTGSSD 51
 RESULT 4
 ADE08993
 ID ADE08993 standard; protein; 95 AA.
 XX
 AC ADE08993;
 XX
 XX 29-JAN-2004 (first entry)
 DT
 XX Novel protein-related config polypeptide sequence #59.
 DE

XX KM novel gene; novel protein; tissue marker; molecular weight marker;
 XX KW chromosome marker; genetic disorder; config.
 XX OS unidentified.
 XX PN WO2003054152-A2.
 XX PD 03-JUL-2003.
 XX PF 10-DEC-2002; 2002WO-US039555.
 XX PR 10-DEC-2001; 2001US-0339739P.
 XX PR 11-DEC-2001; 2001US-0339453P.
 XX PR 14-MAR-2002; 2002US-0365091P.
 XX PR 14-MAR-2002; 2002US-0365384P.
 XX PR 12-APR-2002; 2002US-0372381P.
 XX PR 12-APR-2002; 2002US-0372615P.
 XX PR 22-APR-2002; 2002US-00128558.
 XX PR 24-APR-2002; 2002US-0376045P.
 XX PA (HYSE-) HYSEQ INC.
 XX PI Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao Q, Wang J;
 XX PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;
 XX PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
 XX DR WPI; 2003-569235/53.
 XX PT New polynucleotides, useful for expressing recombinant proteins for
 PT analysis, characterization or therapeutic use, or as markers for tissues
 PT in which the corresponding protein is preferentially expressed.
 XX PS Disclosure; SEQ ID NO 2537; 1177bp; English.
 XX XX The invention comprises the amino acid and coding sequences of novel
 CC proteins. The DNA and protein sequences of the invention are useful as:
 CC markers for tissues in which the corresponding protein is preferentially
 CC expressed; as molecular weight markers on gels; as chromosome markers or
 CC tags; to identify chromosomes or to map related gene positions; and to
 CC compare with endogenous DNA sequences in patients to identify potential
 CC genetic disorders. The present amino acid sequence was used in the
 CC exemplification of the invention.
 XX SQ Sequence 95 AA:
 QY Query Match 25.7%; Score 28; DB 7; Length 95;
 DB Best Local Similarity 100.0%; Pred. No. 1.4e-19;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 QSALTQPASVSGSPGSGITISCTGSSD 28
 24 QSALTQPASVSGSPGSGITISCTGSSD 51
 RESULT 5
 AAR38596
 ID AAR38596 standard; peptide; 104 AA.
 XX
 AC AAR38596;
 XX
 XX 25-MAR-2003 (revised)
 DT 28-OCT-1993 (first entry)
 XX
 XX Human lambda light chain subgroup 4 (HL4).
 DE
 XX Antibody; variable domain; light; L; heavy; H; consensus; affinity;
 KW antigen; immunogenicity; humanisation; framework.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 1
 FT

XX 01-APR-2003 (first entry)
 XX Human lambda chain 2a2:JH2 amino acid sequence #1.
 DE Focused library; genetic package; antibody; kappa light chain; CDR;
 XX lambda light chain; heavy chain; complementary determining region;
 XX diversity.
 OS Homo sapiens.
 OS Synthetic.
 XX MO200261071-A2.
 XX 08-AUG-2002.
 XX 18-DEC-2001; 2001WO-US050297.
 XX 18-DEC-2000; 2000US-0256380P.
 XX (LADN/) LADNER R C.
 XX LADNER RC;
 XX WPI; 2003-067343/06.
 XX Focused library of vectors or genetic packages for displaying or
 PT expressing diversity of an antibody family; comprise variegated DNA
 PT sequences encoding heavy, kappa or lambda light chain complementary
 PT determining regions.
 XX Disclosure; Page 71-72; 92pp; English.
 XX The present invention describes a focused library of vectors or genetic
 CC packages that display, display and express, or comprise a member of a
 CC diverse family of human antibody related peptides, polypeptides and
 CC proteins and collectively display, display or express, or comprise a
 CC portion of the diversity of the antibody family; the vectors or genetic
 CC packages being characterised by variegated DNA sequences that encode a
 CC heavy chain, kappa or lambda light chain complementary determining region
 CC 1 (CDR1), CDR2 or CDR3. The focused library of vectors or genetic
 CC packages of the present invention are useful for displaying, or
 CC displaying and expressing the focused diversity of the family. The
 CC present invention, as compared to prior art, is less time consuming, more
 CC efficient and less cumbersome in the construction of libraries of vectors
 CC and genetic packages using diverse but focused populations of DNA
 CC sequences. ABP56771 to ABP56818 and AB222680 to AB222747 represent
 CC sequences used in the exemplification of the present invention
 XX Sequence 27 AA;
 SQ
 Query Match 21.1%; Score 23; DB 6; Length 27;
 Best Local Similarity 100.0%; Pred. No. 3.9e-15;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QSALTQPAVSQSPGQSIRISCT 23
 DB 3 QSALTQPAVSQSPGQSIRISCT 25
 RESULT 8
 AAU70414
 ID AAU70414 standard; peptide; 22 AA.
 XX AAU70414;
 XX 14-FEB-2002 (first entry)
 DE Human light chain immunoglobulin framework region 1 #6.
 XX Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
 XX complementarity determining region; framework region; IGBP;
 XX transgenic plant; immunoglobulin binding protein array; IGM, IGG, IGA;

KM IGD; IGE; IGY; IGM; kappa; lambda; CHBP.
 XX Homo sapiens.
 OS WO200183806-A1.
 XX 08-NOV-2001.
 XX 02-MAY-2001; 2001WO-US014349.
 XX 02-MAY-2000; 2000US-00563222.
 XX (EPIC-) EPICYTE PHARM INC.
 XX Hiatt AC, Hein MB;
 XX WPI; 2002-055482/07.
 XX The invention relates to transforming a population of cells (e.g. plant
 CC cells), comprising using a library of two different polynucleotides
 CC encoding different immunoglobulin binding protein (IGBP) polypeptides
 CC that specifically bind to a ligand or form one or more disulphide bonds
 CC with polypeptides in transfected cells, to generate an IGBP that binds to
 CC a ligand, and transformed plant cells are selected, and preparing an IGBP
 CC array in plant cells. At least one peptide sequence has at least 75%
 CC sequence identity to a framework region (FR) of a native IGM, IGG, IGA,
 CC IGD, IGE, IGY, kappa or lambda immunoglobulin molecule. The method is
 CC useful for preparing an immunoglobulin binding protein array, preferably
 CC heavy chain binding protein (CHBP) array in eukaryotic cells especially
 CC plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic
 CC cells (e.g. insect cells or mammalian cells). The CHBP is useful for
 CC discovery of e.g. screening assays of IGBPs having desired
 CC characteristics. The present sequence is a mammalian immunoglobulin
 CC derived peptide that may be incorporated into an IGBP of the invention
 XX Sequence 22 AA;
 SQ
 Query Match 20.2%; Score 22; DB 5; Length 22;
 Best Local Similarity 100.0%; Pred. No. 3.1e-14;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QSALTQPAVSQSPGQSIRISC 22
 DB 1 QSALTQPAVSQSPGQSIRISC 22
 RESULT 9
 AAR22580
 ID AAR22580 standard; protein; 94 AA.
 XX AAR22580;
 XX 21-MAY-1992 (first entry)
 DE Light chain VL16.1 from lysozyme binding scFv fragment.
 XX Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat; pilus;
 XX 93p; binding; adsorption; gene VIII; diverse repertoire;
 KM specific binding pairs; replicable genetic display package; human.
 XX Homo sapiens.
 OS WO9201047-A.
 XX WO9201047-A.
 XX 23-JAN-1992.

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PF 10-JUN-1990; 90GB-00015198.
XX
XX 10-JUL-1990; 90GB-00015198.
PR 19-OCT-1990; 90GB-00022845.
PR 12-NOV-1990; 90GB-00024503.
PR 06-MAR-1991; 91GB-00004744.
PR 15-MAY-1991; 91GB-00010549.
XX
XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PA (MEDI-) MED RES COUNCIL.
XX
XX McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
PI Jackson RH, Holliger KP, Marks JD;
XX
XX WPI; 1992-056862/07.
XX
XX Producing members of specific binding pairs - by expression in
PT recombinant host cells with a secreting replicable genetic display
PT package.
XX
XX Table 11; Page 152; 209pp; English.
XX
XX PCR was used to prepare a human scFv library from RNA from white blood
XX cells from an unimmunised donor. Heavy chains from Igg and Igm antibodies
XX were amplified separately. Four separate libraries were generated (Igg-K,
XX Igg-Lambda, Igm-K and Igm-Lambda). The purified scFv fragments were
XX ligated into the phagemid pHEM1 for expression on the surface of fd
XX bacteriophage as gene III fusions. The clones were then subjected to
XX affinity selection for binding to lysozyme by selection on tubes followed
XX by analysis by ELISA. 50 positive lysozyme binding clones were
XX identified, >95% being from the Igm library. The clones gave three
XX different BstNI restriction patterns, and at least 2 clones from each
XX pattern were sequenced. The sequences indicated the presence of 4 unique
XX human VH-VL combinations. The sequence shown here is one of the light
XX chains found. See also AAR21260-307, 309-312, AAR22450, AAR22565,
XX AAR22567-81
XX
XX Sequence 94 AA;
SQ
Query Match 20.2%; Score 22; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 1.1e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QSALTDPASVSGSPGQSITISC 22
Db 1 QSALTDPASVSGSPGQSITISC 22

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PR 09-JUN-1999; 99GB-00013435.
XX
XX (MEDI-) MEDICAL RES COUNCIL.
XX
XX Sale JE, Neuberger MS, Cumbers SJ;
PI WPI; 2000-317971/27.
XX
XX N-PSDB; AAS2443.
XX
XX Lymphoid cell line preparation useful for producing gene products having
PT desired activity, involves screening and selecting cells having ongoing
PT target sequence diversification and higher mutation rates.
XX
XX Example 5; Fig 11; 69pp; English.
XX
XX The invention relates to a method of preparing a lymphoid cell line
XX capable of capable of directed constitutive hypermutation of a target
XX nucleic acid region. The method comprises screening a cell population for
XX ongoing target sequence diversification and selecting a cell in which the
XX rate of target nucleic acid mutation exceeds that of other nucleic acid
XX mutation by a factor of 100 or more. The invention also relates to a
XX method for preparing a gene product with a desired activity, comprising
XX expressing a nucleic acid encoding the target gene operably linked to a
XX sequence which directs hypermutation e.g., terminal deoxynucleotidyl
XX transferase (TdT), in the lymphoid cell line, and identifying a cell or
XX cells which express a mutated gene product with the desired activity. One
XX or more clonal populations of the identified cells is established, and
XX cells with an improved activity of interest are selected. These steps may
XX be iteratively repeated until a gene product with a desired activity
XX is obtained. The cell lines prepared according to the method of the
XX invention are used for directed constitutive hypermutation of a nucleic
XX acid region in the preparation of a gene product, preferably an enzyme or
XX an immunoglobulin (Ig) with a desired activity. In the exemplifications
XX of the invention, Igm-secreting Ramos cells were selected for use as they
XX undergo hypermutation during clonal expansion. The present sequence
XX represents the wild-type Ramos cell light chain variable region (VL)
XX
XX Sequence 100 AA;
SQ
Query Match 20.2%; Score 22; DB 3; Length 100;
Best Local Similarity 100.0%; Pred. No. 1.2e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 PASVSGSPGQSITISCTGTSSD 28
Db 1 PASVSGSPGQSITISCTGTSSD 22

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PR 09-OCT-1998; 98GB-00022104.
 PR 19-JAN-1999; 99GB-00001141.
 PR 09-JUN-1999; 99GB-00013435.
 PA (MEDI-) MEDICAL RES COUNCIL.
 PI Sale JE, Neuberger MS, Cumbers SJ;
 DR WPI; 2000-317971/27.
 DR N-PSDB; AAA52446.
 XX
 PT Lymphoid cell line preparation useful for producing gene products having
 PT desired activity, involves screening and selecting cells having ongoing
 PT target sequence diversification and higher mutation rates.
 PS
 XX Example 5; Fig 16; 69pp; English.

CC The invention relates to a method of preparing a lymphoid cell line
 CC capable of capable of directed constitutive hypermutation of a target
 CC nucleic acid region. The method comprises screening a cell population for
 CC ongoing target sequence diversification and selecting a cell in which the
 CC rate of target nucleic acid mutation exceeds that of other nucleic acid
 CC mutation by a factor of 100 or more. The invention also relates to a
 CC method for preparing a gene product with a desired activity, comprising
 CC expressing a nucleic acid encoding the target gene operably linked to a
 CC sequence which directs hypermutation e.g., terminal deoxynucleotidyl
 CC transferase (Tdt), in the lymphoid cell line, and identifying a cell or
 CC cells which express a mutated gene product with the desired activity. One
 CC or more clonal populations of the identified cells is established, and
 CC cells with an improved activity of interest are selected. These steps may
 CC be iteratively repeated until a gene product with a desired activity
 CC is obtained. The cell lines prepared according to the method of the
 CC invention are used for directed constitutive hypermutation of a nucleic
 CC acid region in the preparation of a gene product, preferably an enzyme or
 CC an immunoglobulin (Ig) with a desired activity. In the exemplifications
 CC of the invention, IgM-secreting Ramos cells were selected for use as they
 CC undergo hypermutation during clonal expansion. The present sequence
 CC represents a mutant IgM light chain variable region (VL) from a Ramos
 CC cell which binds streptavidin with high affinity. The cell is the product
 CC of 6 rounds of clonal expansion, hypermutation and selection
 CC
 XX
 SQ Sequence 100 AA;

Query Match 20.2%; Score 22; DB 3; Length 100;
 Best Local Similarity 100.0%; Pred. No. 1.2e-13;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PASVSGSPQGSITISCTGTSSD 28
 |||||
 DB 1 PASVSGSPQGSITISCTGTSSD 22

RESULT 12
 AAB53507
 ID AAB53507 standard; protein; 92 AA.
 AC AAB53507;
 XX
 DT 09-MAR-2001 (first entry)
 XX
 DE Human colon cancer antigen protein sequence SEQ ID NO:1047.
 XX
 KM Human; colon cancer; colon cancer antigen; diagnosis; detection;
 KM identification; cytostatic; cardioactive; neuroprotective; vulnary;
 KM immunomodulatory; muscular; gynaecological; gastrointestinal;
 KM nephrotropic; antiinfective; antibacterial; gene therapy; wound;
 KM neural disorder; immune system disorder; muscular disorder;
 KM reproductive disorder; gastrointestinal disorder; renal disorder;
 KM infectious disease; cardiovascular disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200055351-A1.

XX
 PD 21-SEP-2000.
 XX
 PF 08-MAR-2000; 2000MO-US005883.
 XX
 PR 12-MAR-1999; 99US-0124270P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Rosen CA, Ruben SM;
 DR WPI; 2000-587534/55.
 DR N-PSDB; AAC98264.
 XX
 PT Colon cancer associated gene sequences, referred to as colon cancer
 PT antigens, useful for the treatment, prevention, and diagnosis of colon
 PT disorders such as colon cancer.
 PS
 XX Claim 11; Page 1627-1628; 2104pp; English.

CC AAC97991 to AAC98763 encode the human colon cancer associated proteins,
 CC called human colon cancer antigens, given in AAB53234 to AAB54006. The
 CC human colon cancer antigens can have cytostatic, cardioactive, muscular;
 CC neuroprotective, immunomodulatory, gynaecological, gastrointestinal,
 CC vulnary, nephrotropic, antiinfective and antibacterial activities, and
 CC can be used in gene therapy. The colon cancer antigen polynucleotides,
 CC proteins and antibodies to the proteins are useful for the prevention,
 CC treatment and diagnosis of colon disorders, such as colon cancer. The
 CC polynucleotides may be used in diagnostics and research, such as for
 CC chromosome identification, and as hybridisation probes. The proteins may
 CC also be used to prevent diseases such as neural disorders, gastrointestinal
 CC disorders, wounds, renal disorders, infectious diseases, and
 CC cardiovascular disorders. AAC98764 to AAC98772 and AAB54007 represent
 CC sequences used in the exemplification of the present invention
 CC
 XX
 SQ Sequence 92 AA;

Query Match 19.3%; Score 21; DB 3; Length 92;
 Best Local Similarity 100.0%; Pred. No. 1.1e-12;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 TASLTISGLQAEDEADYCCS 92
 |||||
 DB 11 TASLTISGLQAEDEADYCCS 31

RESULT 13
 ABB39374
 ID ABB39374 standard; peptide; 97 AA.
 XX
 AC ABB39374;
 XX
 DT 04-FEB-2002 (first entry)
 XX
 DE Peptide #6880 encoded by human foetal liver single exon probe.
 XX
 KM Human; foetal liver; gene expression; single exon nucleic acid probe.
 KM
 OS Homo sapiens.
 XX
 PN WO200157277-A2.
 XX
 DE 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000669.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-0060840P.
 PR 03-AUG-2000; 2000US-0063236P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483447/52.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human fetal liver.
XX
XX Claim 27; SEQ ID NO 32009; 639pp + Sequence Listing; English.
XX
XX The invention relates to a single exon nucleic acid probe for measuring
CC human gene expression in a sample derived from human foetal liver. The
CC single exon nucleic acid probes may be used for predicting, measuring and
CC displaying gene expression in samples derived from human fetal liver. The
CC present sequence is a peptide encoded by a single exon nucleic acid probe
CC of the invention. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
CC
XX Sequence 97 AA;
SQ
Query Match 19.3%; Score 21; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.1e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 8 ASVSGSPGQSITISCTGTSSD 28
Db 1 ASVSGSPGQSITISCTGTSSD 21
RESULT 14
AAM32889
ID AAM32889 standard; protein: 97 AA.
XX
XX AAM32889;
XX
XX 17-OCT-2001 (first entry)
XX Peptide #6926 encoded by probe for measuring placental gene expression.
XX
XX Probe; microarray; human; placenta; antenatal diagnosis;
XX Genetic disorder.
XX
XX Homo sapiens.
XX
XX WO200157272-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000663.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488897/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human placenta.
XX
XX Claim 27; SEQ ID NO 33158; 654pp; English.
XX

CC The present invention relates to single exon nucleic acid probes (SENPs;
CC see AAI31315-AA157546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders
XX
XX Sequence 97 AA;
SQ
Query Match 19.3%; Score 21; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.1e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 8 ASVSGSPGQSITISCTGTSSD 28
Db 1 ASVSGSPGQSITISCTGTSSD 21
RESULT 15
ABB24161
ID ABB24161 standard; protein: 97 AA.
XX
XX ABB24161;
XX
XX 23-JAN-2002 (first entry)
XX
XX Protein #6160 encoded by probe for measuring heart cell gene expression.
XX
XX Human; gene expression; heart; microarray; vascular system;
XX cardiovascular disease; hypertension; cardiac arrhythmia;
XX congenital heart disease.
XX
XX Homo sapiens.
XX
XX WO200157274-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000666.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488899/53.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
PT hearts.
XX
XX Claim 15; SEQ ID NO 25931; 530pp; English.
XX
XX The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart (see
CC ABA21535-ABA41305). The present sequence is a protein encoded by one such
CC probe. The probes may be used for predicting, measuring and displaying
CC gene expression in samples derived from the human heart via microarrays.
CC By measuring gene expression, the probes are useful for predicting, the
CC diagnosing, grading, staging, monitoring and prognosing diseases of the
CC human heart and vascular system e.g. cardiovascular disease,
CC hypertension, cardiac arrhythmias and congenital heart disease. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 97 AA;
SQ

Query Match 19.3%; Score 21; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.1e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 ASVSGSPGQSTIRISCTGTSSD 28
DB 1 ASVSGSPGQSTIRISCTGTSSD 21

RESULT 16
AAM72656
ID AAM72656 standard; protein; 97 AA.

XX AAM72656;

XX 06-NOV-2001 (first entry)

XX Human bone marrow expressed probe encoded protein SEQ ID NO: 32962.

XX Human; bone marrow expressed exon; gene expression analysis; probe;

XX microarray; cancer; leukaemia; lymphoma; myeloma.

XX Homo sapiens.

XX WO200157276-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000668.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488900/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

XX gene expression in human bone marrow.

XX Example 4; SEQ ID NO 32962; 656bp + Sequence Listing; English.

XX The present invention provides a number of single exon nucleic acid

XX probes which are derived from genomic sequences expressed in the human

XX bone marrow. They can be used to measure gene expression in bone marrow

XX samples, which may enable the improved diagnosis and treatment of cancers

XX such as lymphoma, leukaemia and myeloma. The present sequence is a

XX protein encoded by one of the probes of the invention

XX Sequence 97 AA;

XX Query Match 19.3%; Score 21; DB 4; Length 97;

XX Best Local Similarity 100.0%; Pred. No. 1.1e-12;

XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 05-NOV-2001 (first entry)

XX Human brain expressed single exon probe encoded protein SEQ ID NO: 32157.

XX Human; brain expressed exon; gene expression analysis; probe; microarray;

XX Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.

XX Homo sapiens.

XX WO200157275-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000667.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-483446/52.

XX Single exon nucleic acid probes for analyzing gene expression in human

XX brains.

XX Example 4; SEQ ID NO 32157; 650bp + Sequence Listing; English.

XX The present invention provides a number of single exon nucleic acid

XX probes which are derived from genomic sequences expressed in the human

XX brain. They can be used to measure gene expression in brain cell samples,

XX which may enable the diagnosis and improved treatment of nervous system

XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,

XX epilepsy and cancers. The present sequence is a protein encoded by one of

XX the probes of the invention

XX Sequence 97 AA;

XX Query Match 19.3%; Score 21; DB 4; Length 97;

XX Best Local Similarity 100.0%; Pred. No. 1.1e-12;

XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 8 ASVSGSPGQSTIRISCTGTSSD 28

XX 1 ASVSGSPGQSTIRISCTGTSSD 21

XX RESULT 16

XX ABG54353

XX ID ABG54353 standard; peptide; 97 AA.

XX 25-FEB-2003 (first entry)

XX Human liver peptide, SEQ ID NO 33001.

XX Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;

XX hypercholesterolaemia; coronary heart disease.

XX Homo sapiens.

XX WO200157273-A2.

XX 09-AUG-2001.

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PF 30-JAN-2001; 2001WO-US000664.
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488898/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human adult liver.
XX
XX Claim 27; SEQ ID NO 33001; 658bp; English.
XX
XX The invention relates to a single exon nucleic acid probe (SENP) (1) for
XX measuring human gene expression in a sample derived from human adult
XX liver, comprising one of 13109 defined nucleotide sequences given in the
XX specification (or complements/ fragments). The probe hybridises at high
XX stringency to a nucleic acid molecule expressed in the human adult liver.
XX (1) may be used for predicting, measuring and displaying gene expression
XX in samples derived from human adult liver. The genes identified may be
XX involved in genetic liver diseases such as cirrhosis,
XX hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
XX associated with coronary heart disease. ABG47348-ABG59930 represent human
XX liver single exon encoded peptides of the invention. Note: The sequence
XX information for this patent does not appear in the printed Specification
XX but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 97 AA:
XX
XX Query Match 19.3%; Score 21; DB 4; Length 97;
XX Best Local Similarity 100.0%; Pred. No. 1.1e-12;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 8 ASVSGSPGQGITISCTGTSSD 28
XX 1 ASVSGSPGQGITISCTGTSSD 21
XX
XX RESULT 19
XX ABG42480
XX ID ABG42480 standard; peptide; 97 AA.
XX
XX ABG42480;
XX
XX 19-AUG-2002 (first entry)
XX
XX Human peptide encoded by genome-derived single exon probe SEQ ID 32145.
XX
XX Human, single exon probe; asthma; lung cancer; COPD; ILD;
XX chronic obstructive pulmonary disease; interstitial lung disease;
XX familial idiopathic pulmonary fibrosis; neurofibromatosis;
XX tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
XX Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
XX pulmonary histiocytosis; lymphangioleiomyomatosis; Karsenger syndrome;
XX pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
XX primary ciliary dyskinesia; pulmonary hypertension;
XX hyaline membrane disease.
XX
XX Homo sapiens.
XX
XX WO200186003-A2.
XX
XX 15-NOV-2001.
XX

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PF 30-JAN-2001; 2001WO-US000665.
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2002-114183/15.
XX
XX Spatially-addressable set of single exon nucleic acid probes, used to
XX measure gene expression in human lung samples.
XX
XX Claim 27; SEQ ID NO 32145; 634bp; English.
XX
XX The invention relates to a spatially-addressable set of single exon
XX nucleic acid probes for measuring gene expression in a sample derived
XX from human lung comprising single exon nucleic acid probes having one of
XX 12614 nucleic acid sequences mentioned in the specification, or their
XX complements or the 12817 open reading frames derived from the 12614
XX probes. Also included are a microarray comprising the novel set of probes
XX; the novel set of probes which hybridise at high stringency to a nucleic
XX acid expressed in the human lung; measuring gene expression in a sample
XX derived from human lung, comprising (a) contacting the array with a
XX collection of detectably labeled nucleic acids derived from human lung
XX mRNA, and (b) measuring the label detectably bound to each probe of the
XX array; identifying exons in a eukaryotic genome, comprising (a)
XX algorithmically predicting at least one exon from genomic sequences of
XX the eukaryote; and (b) detecting specific hybridisation of detectably
XX labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
XX having a fragment identical to the predicted exon, the probe is included
XX in the above mentioned microarray; assigning exons to a single gene,
XX comprising (a) identifying exons from genomic sequence by the method
XX above and (b) measuring the expression of each of the exons in several
XX tissues and/or cell types using hybridisation to a single exon
XX microarrays having a probe with the exon, where a common pattern of
XX expression of the exons in the tissues and/or cell types indicates that
XX the exons should be assigned to a single gene; a peptide comprising one
XX of 12011 sequences, mentioned in the specification, or encoded by the
XX probes/open reading frames (ORF). The probes are used for gene expression
XX analysis, and for identifying exons in a gene, particularly using human
XX lung derived mRNA and for the study of lung diseases such as asthma, lung
XX cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
XX disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
XX tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
XX Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
XX histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
XX Karsenger syndrome, fibrocystic pulmonary dysplasia, primary ciliary
XX dyskinesia, pulmonary hypertension and hyaline membrane disease. The
XX present sequence is a peptide/protein encoded by a single exon probe of
XX the invention. Note: The sequence data for this patent did not form part
XX of the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 97 AA:
XX
XX Query Match 19.3%; Score 21; DB 5; Length 97;
XX Best Local Similarity 100.0%; Pred. No. 1.1e-12;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 8 ASVSGSPGQGITISCTGTSSD 28
XX 1 ASVSGSPGQGITISCTGTSSD 21
XX
XX RESULT 20
XX AAR22579
XX

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ID AAR22579 standard; protein; 103 AA.
 XX
 AC AAR22579;
 XX
 DT 21-MAY-1992 (first entry)
 XX
 DE Light chain VLJ3.1 from lysozyme binding scFv fragment.
 XX
 KM Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat; pilus;
 KM G3P; binding; adsorption; gene VIII; diverse repertoire;
 KM specific binding pairs; replicable genetic display package; human.
 XX
 OS Homo sapiens.
 XX
 PN WO9201047-A.
 XX
 PD 23-JAN-1992.
 XX
 PF 10-JUL-1990; 90GB-00015198.
 XX
 PR 10-JUL-1990; 90GB-00015198.
 PR 19-OCT-1990; 90GB-00022845.
 PR 12-NOV-1990; 90GB-00024503.
 PR 06-MAR-1991; 91GB-00004744.
 PR 15-MAY-1991; 91GB-00010549.
 XX
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 PA (MEDI-) MED RES COUNCIL.
 XX
 PI McCaferry J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
 PI Jackson RH, Holliger KP, Marks JD;
 XX
 DR WPI; 1992-056862/07.
 XX
 PT Producing members of specific binding pairs - by expression in
 PT recombinant host cells with a secreting replicable genetic display
 PT package.
 XX
 PS Table 11; Page 152; 209pp; English.
 XX
 XX PCR was used to prepare a human scFv library from RNA from white blood
 CC cells from an unimmunised donor. Heavy chains from Igg and Igm antibodies
 CC were amplified separately. Four separate libraries were generated (Igg-X,
 CC Igg-lambda, Igm-X and Igm-lambda). The purified scFv fragments were
 CC ligated into the phagemid PHEN1 for expression on the surface of fd
 CC bacteriophage as gene III fusions. The clones were then subjected to
 CC affinity selection for binding to lysozyme by selection on tubes followed
 CC by analysis by ELISA. 50 positive lysozyme binding clones were
 CC identified, >95% being from the Igm library. The clones gave three
 CC different BstNI restriction patterns, and at least 2 clones from each
 CC pattern was sequenced. The sequences indicated the presence of 4 unique
 CC human VH-VL combinations. The sequence shown here is one of the light
 CC chains found. See also AAR21260-307, 309-312, AAR22450, AAR22565,
 CC AAR22567-81
 CC
 SQ Sequence 103 AA;
 XX
 Query Match 19.3%; Score 21; DB 2; Length 103;
 Best Local Similarity 100.0%; Pred. No. 1.2e-12;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX
 DE Human light chain immunoglobulin framework region 3 #6.
 XX
 KM Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
 KM complementarity determining region; framework region; IGBP;
 KM transgenic plant; immunoglobulin binding protein array; Igm; Igg; Iga;
 KM Igd; Ige; Igy; Igm; kappa; lambda; CHBP.
 XX
 OS Homo sapiens.
 XX
 PN WO200183806-A1.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US014349.
 XX
 PR 02-MAY-2000; 2000US-00563222.
 XX
 PA (EPIC-) EPICYTE PHARM INC.
 XX
 PI Hiatt AC, Hein MB;
 XX
 DR WPI; 2002-055482/07.
 XX
 PT Preparing immunoglobulin binding protein array in plant cells by
 PT transforming the cells with different polynucleotides encoding binding
 PT protein polypeptides specific to ligand, selecting plant cells for
 PT preparing array.
 XX
 PS Disclosure; Fig 1A; 129pp; English.
 XX
 CC The invention relates to transforming a population of cells (e.g. plant
 CC cells), comprising using a library of two different polynucleotides
 CC encoding different immunoglobulin binding protein (IGBP) polypeptides
 CC that specifically bind to a ligand or form one or more disulphide bonds
 CC with polypeptides in transfected cells, to generate an IGBP that binds to
 CC a ligand, and transformed plant cells are selected, and preparing an IGBP
 CC array in plant cells. At least one peptide sequence has at least 75%
 CC sequence identity to a framework region (FR) of a native Igm, Igg, Iga,
 CC Igd, Ige, Igy, kappa or lambda immunoglobulin molecule. The method is
 CC useful for preparing an immunoglobulin binding protein array, preferably
 CC heavy chain binding protein (CHBP) array in eukaryotic cells especially
 CC plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic
 CC cells (e.g. insect cells or mammalian cells). The CHBP is useful for
 CC discovery of e.g. screening assays of IGBPs having desired
 CC characteristics. The present sequence is a mammalian immunoglobulin
 CC derived peptide that may be incorporated into an IGBP of the invention
 CC
 SQ Sequence 32 AA;
 XX
 Query Match 17.4%; Score 19; DB 5; Length 32;
 Best Local Similarity 100.0%; Pred. No. 3.9e-11;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 TASLTISGLQAEADYYC 90
 DB 14 TASLTISGLQAEADYYC 32

RESULT 22
 AAB84353
 ID AAB84353 standard; protein; 103 AA.
 XX
 AC AAB84353;
 XX
 DT 22-AUG-2001 (first entry)
 XX
 DE Amino acid sequence of light chain of intrabody ST6/34.
 XX
 KM Surface receptor-dependent infection; pathogenic agent; antibody;
 KM intrabody; ST6/34; chemokine receptor; CCR5.
 XX
 OS Oryctolagus cuniculus.

XX WO200142308-A2.
XX 14-JUN-2001.
XX 08-DEC-2000; 2000WO-EP012419.
XX 08-DEC-1999; 99US-0169653P.
XX (NOVS) NOVARTIS AG.
XX (SCRI) SCRIPPS RES INST.
XX Barbas CF, Steindorger P;
XX WPI; 2001-381649/40.
XX Inhibiting, preventing or treating pathogenic infection of cells
PT comprises expressing recombinant antibody specific for surface receptor
PT of cells necessary for pathogenic infection, fused to intracellular
PT anchor means.
XX Claim 1; Page 58; 69pp; English.
XX The specification describes a method for inhibiting, diminishing,
CC preventing or treating surface receptor-dependent infection of cells by
CC pathogenic agents. The method comprises a recombinant antibody protein
CC fused to an intracellular anchor means, where the antibody is specific
CC for a surface receptor of the cells necessary for pathogenic infection.
CC The anchor means may be an endoplasmic reticulum retention peptide. The
CC present sequence represents the light chain of the antibody S16/34,
CC which is specific for the chemokine receptor CCR5. The present protein is
CC used to produce antibody proteins of the invention
XX Sequence 103 AA;
SQ
Query Match 17.4%; Score 19; DB 4; Length 103;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 72 TASLTISGQAEDEADYYC 90
DB 69 TASLTISGQAEDEADYYC 87
RESULT 23
AAR88719
ID AAR88719 standard; protein; 108 AA.
XX AAR88719;
XX 26-SEP-1996 (first entry)
XX Human antibody lambda chain variable region consensus sequence.
XX Antibody; stability; instability; mutagenesis; amino acid frequency;
XX canonical sequence approximation; substitution; immunoglobulin;
XX light chain; variable region; VL-region; diagnosis; immunoassay;
XX cancer treatment; autoimmune disease; immunotoxin; improved yield.
XX Homo sapiens.
XX OS
XX DE4425115-A1.
XX 18-JAN-1996.
XX 15-JUL-1994; 94DE-04425115.
XX 15-JUL-1994; 94DE-04425115.
XX (BOEF) BOEHRINGER MANNHEIM GMBH.
XX Steipe B, Steinbacher S;
XX

DR WPI; 1996-069594/08.
XX Functional antibodies modified to increase or decrease stability - have
PT specific amino acid substns. in the variable domain, determined by
PT reference to consensus sequences.
XX Claim 2; Page 31; 43pp; German.
XX Consensus sequences were established for antibody variable regions from
CC human and mouse heavy and light (kappa and lambda) chains. In addition,
CC frequency tables listing the amino acids which can be found at each
CC position were compiled. In a new method, mutations are introduced into an
CC antibody variable domain by reference to the frequency table. When an
CC amino acid is replaced by one which occurs at a higher frequency at that
CC position, the resulting antibody chain is more stable than the wild-type;
CC when an amino acid is replaced by one which occurs less frequently (or
CC not at all), the resulting antibody is less stable than the wild-type.
CC Stabilised antibodies are useful as diagnostic reagents, as catalysts and
CC in treatment of cancer, autoimmune diseases and infections. Destabilised
CC antibodies have improved (faster) pharmacokinetic properties. The present
CC sequence is the human lambda light chain variable region consensus
CC sequence
XX Sequence 108 AA;
SQ
Query Match 17.4%; Score 19; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 72 TASLTISGQAEDEADYYC 90
DB 69 TASLTISGQAEDEADYYC 87
RESULT 24
AAB01958
ID AAB01958 standard; protein; 100 AA.
XX AAB01958;
XX 18-SEP-2000 (first entry)
XX Streptavidin-binding mutant Ramos cell VL.
XX Lymphoid cell; antibody producing cell; Ramos cell; immunoglobulin M;
XX IGM; V gene diversity; directed constitutive hypermutation;
XX target sequence diversification; terminal deoxynucleotidyl transferase;
XX TdT; clonal expansion; selection; light chain variable region; VL;
XX streptavidin binding; mutant; mutain.
XX Homo sapiens.
XX OS
XX Synthetic.
XX WO200022111-A1.
XX 20-APR-2000.
XX 08-OCT-1999; 99WO-GB003358.
XX 09-OCT-1998; 98GB-00022104.
XX 19-JAN-1999; 99GB-00001141.
XX 09-JUN-1999; 99GB-00013435.
XX (MEDT-) MEDICAL RES COUNCIL.
XX Sale JE, Neuberger MS, Cumbers SJ;
XX WPI; 2000-317971/27.
XX N-PSDB; AA52444.
XX Lymphoid cell line preparation useful for producing gene products having
PT desired activity, involves screening and selecting cells having ongoing
PT target sequence diversification and higher mutation rates.
XX

XX Example 5; Fig 11; 69pp; English.

CC The invention relates to a method of preparing a lymphoid cell line
 CC capable of capable of directed constitutive hypermutation of a target
 CC nucleic acid region. The method comprises screening a cell population for
 CC ongoing target sequence diversification and selecting a cell in which the
 CC rate of target nucleic acid mutation exceeds that of other nucleic acid
 CC mutation by a factor of 100 or more. The invention also relates to a
 CC method for preparing a gene product with a desired activity, comprising
 CC expressing a nucleic acid encoding the target gene operably linked to a
 CC sequence which directs hypermutation e.g., terminal deoxynucleotidyl
 CC transferase (Tdt), in the lymphoid cell line, and identifying a cell or
 CC cells which express a mutated gene product with the desired activity. One
 CC or more clonal populations of the identified cells is established, and
 CC cells with an improved activity of interest are selected. These steps may
 CC be iteratively repeated until a gene product with a desired of activity
 CC is obtained. The cell lines prepared according to the method of the
 CC invention are used for directed constitutive hypermutation of a nucleic
 CC acid region in the preparation of a gene product, preferably an enzyme or
 CC an immunoglobulin (Ig) with a desired activity. In the exemplifications
 CC of the invention, IgM-secreting Ramos cells were selected for use as they
 CC undergo hypermutation during clonal expansion. The present sequence
 CC represents a mutant IgM light chain variable region (V_L) from a Ramos
 CC cell which binds streptavidin. The cell is the product of 4 rounds of
 CC clonal expansion, hypermutation and selection

SQ Sequence 100 AA;

Query Match 15.6%; Score 17; DB 3; Length 100;
 Best Local Similarity 100.0%; Pred. No. 1e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GSPGQSITISCTGTSSD 28
 |||||
 Db 6 GSPGQSITISCTGTSSD 22

RESULT 25
 AAG93626
 ID AAG93626 standard; protein; 104 AA.
 XX
 AC AAG93626;

DT 14-SEP-2001 (first entry)
 XX
 DE Human anti-Rh(D) chain S01 protein sequence.

KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
 red blood cell; Rh phenotype; diagnosis; therapeutic.

OS Homo sapiens.

PN US6255455-B1.

PD 03-JUL-2001.

PF 29-JAN-1999; 99US-00240274.

PR 11-OCT-1996; 96US-0028550P.

PR 27-JUN-1997; 97US-0084045.

PR 10-APR-1998; 98US-0081380P.

PA (TYPE-) UNIV PENNSYLVANIA.

PI Siegel DJ;

WPI; 2001-388931/41.

DR N-PSDB; AAH68683.

PT New isolated protein, preferably a human anti-Rh(D) antibody for use in
 PT diagnostics requiring a human instead of an animal antibody and in
 PT therapeutic medicine.

XX Claim 1; Col 46; 162pp; English.

CC The present invention describes an isolated Rh(D) binding protein,
 CC preferably a human antibody, (I) having an amino acid sequence comprising
 CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
 CC immunostimulant activity, and can be used as an immune system stimulant.
 CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
 CC are used in diagnostics that require human antibodies instead of animal
 CC antibodies, such as determine the Rh phenotype of human red blood cells.
 CC AAG93558 to AAG93669 represent the nucleotide sequence which encode
 CC chain CDR3 amino acid sequences which are given in the exemplification of
 CC the present invention

SQ Sequence 104 AA;

Query Match 15.6%; Score 17; DB 4; Length 104;
 Best Local Similarity 100.0%; Pred. No. 1e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 TASITISGLQAEDEADY 88
 |||||
 Db 67 TASITISGLQAEDEADY 83

Search completed: March 15, 2004, 07:42:05
 Job time : 57 secs

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OM protein - protein search, using sw model

Run on: March 15, 2004, 07:40:59 / Search time 23 Seconds
(without alignments)
244.662 Million cell updates/sec

Title: US-09-620-955b-4

Perfect score: 109

Sequence: 1 OSALTOPASVSGSPGOSITL.....CSSFANSGPLFGGTRKTVTL 109

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 389414 seqs, 51625971 residues
Word size: 0
Total number of hits satisfying chosen parameters: 270590

Minimum DB seq length: 0
Maximum DB seq length: 109

Post-processing: Listing first 100 summaries

Database: Issued: Patents/AA:***
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2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
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6: /cgn2_6/ptodata/2/1aa/backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	23.9	104	1	US-08-488-113B-153
2	26	23.9	104	1	US-08-477-484B-153
3	26	23.9	104	1	US-08-107-668D-17
4	26	23.9	104	1	US-08-472-788A-17
5	26	23.9	104	2	US-08-477-531B-17
6	26	23.9	104	2	US-08-646-360-153
7	26	23.9	104	2	US-08-082-842A-17
8	26	23.9	104	3	US-08-839-765-153
9	26	23.9	104	3	US-09-136-389-153
10	26	23.9	104	4	US-09-610-838-153
11	26	23.9	104	4	US-09-711-485-153
12	19	17.4	64	2	US-08-765-179B-19
13	19	17.4	109	3	US-09-157-370-5
14	17	15.6	104	3	US-09-240-274-69
15	17	15.6	108	3	US-09-240-274-68
16	17	11.0	103	1	US-07-942-245-8
17	12	11.0	103	1	US-08-107-668D-3
18	12	11.0	103	1	US-08-472-788A-3
19	12	11.0	103	2	US-08-477-531B-3
20	12	11.0	103	2	US-08-082-842A-3
21	12	11.0	103	3	US-08-992-176-3
22	12	11.0	104	3	US-09-240-274-49
23	11	10.1	64	3	US-08-765-179B-10
24	11	10.1	76	3	US-08-851-362D-20
25	11	10.1	95	2	US-08-290-592E-19
26	11	10.1	95	2	US-08-290-592E-33
27	11	10.1	95	5	PCT-US95-10053-16

28	11	10.1	95	5	PCT-US95-10053-30	Sequence 30, Appl
29	11	10.1	95	5	PCT-US96-09448-19	Sequence 19, Appl
30	11	10.1	95	5	PCT-US96-09448-33	Sequence 33, Appl
31	11	10.1	96	1	US-08-488-113B-158	Sequence 158, App
32	11	10.1	96	1	US-08-477-484B-158	Sequence 158, App
33	11	10.1	96	1	US-08-472-788A-22	Sequence 22, Appl
34	11	10.1	96	2	US-08-477-531B-22	Sequence 22, Appl
35	11	10.1	96	2	US-08-646-360-158	Sequence 158, App
36	11	10.1	96	2	US-08-082-842A-22	Sequence 22, Appl
37	11	10.1	96	3	US-08-839-765-158	Sequence 158, App
38	11	10.1	96	3	US-09-136-389-158	Sequence 158, App
39	11	10.1	96	4	US-09-610-838-158	Sequence 158, App
40	11	10.1	96	4	US-09-711-485-158	Sequence 158, App
41	11	10.1	105	3	US-08-851-362D-28	Sequence 28, Appl
42	11	10.1	105	3	US-08-851-362D-38	Sequence 38, Appl
43	11	10.1	106	3	US-07-634-278-35	Sequence 35, Appl
44	11	10.1	106	1	US-07-634-278-35	Sequence 35, Appl
45	11	10.1	106	1	US-08-477-728-35	Sequence 35, Appl
46	11	10.1	106	1	US-08-477-728-35	Sequence 35, Appl
47	11	10.1	106	1	US-08-474-040-59	Sequence 59, Appl
48	11	10.1	106	1	US-08-474-040-59	Sequence 59, Appl
49	11	10.1	106	1	US-08-487-200-35	Sequence 35, Appl
50	11	10.1	106	1	US-08-487-200-59	Sequence 59, Appl
51	11	10.1	106	3	US-08-484-537-35	Sequence 35, Appl
52	11	10.1	106	3	US-08-484-537-35	Sequence 35, Appl
53	11	10.1	106	3	US-08-619-491-9	Sequence 9, Appl
54	11	10.1	106	4	US-09-771-415-17	Sequence 17, Appl
55	11	10.1	106	4	US-09-771-415-17	Sequence 17, Appl
56	11	10.1	106	4	US-09-771-415-19	Sequence 19, Appl
57	11	10.1	106	4	US-09-771-415-21	Sequence 21, Appl
58	11	10.1	106	4	US-09-771-415-23	Sequence 23, Appl
59	11	10.1	106	4	US-09-771-415-25	Sequence 25, Appl
60	11	10.1	106	5	PCT-US95-07302-9	Sequence 9, Appl
61	11	10.1	107	1	US-08-276-852-107	Sequence 107, App
62	11	10.1	107	1	US-08-276-852-107	Sequence 107, App
63	11	10.1	107	1	US-08-899-575-107	Sequence 108, App
64	11	10.1	107	1	US-08-899-575-108	Sequence 108, App
65	11	10.1	107	1	US-08-899-575-108	Sequence 108, App
66	11	10.1	107	1	US-08-899-575-108	Sequence 108, App
67	11	10.1	107	2	US-08-303-569B-25	Sequence 25, Appl
68	11	10.1	107	2	US-08-070-116A-8	Sequence 8, Appl
69	11	10.1	107	2	US-08-116-247-26	Sequence 26, Appl
70	11	10.1	107	2	US-08-557-050-8	Sequence 8, Appl
71	11	10.1	107	4	US-09-795-515-25	Sequence 25, Appl
72	11	10.1	107	4	PCT-US95-08743-107	Sequence 107, App
73	11	10.1	107	5	PCT-US95-08743-108	Sequence 108, App
74	11	10.1	109	3	US-09-157-370-3	Sequence 3, Appl
75	11	10.1	109	3	US-08-466-368-13	Sequence 13, Appl
76	10	9.2	13	3	US-08-470-998-10	Sequence 10, Appl
77	10	9.2	13	4	US-08-328-500-18	Sequence 18, Appl
78	10	9.2	15	1	US-07-946-421-8	Sequence 8, Appl
79	10	9.2	15	1	US-08-137-117D-121	Sequence 121, App
80	10	9.2	15	1	US-08-137-117D-140	Sequence 140, App
81	10	9.2	15	2	US-08-436-717-140	Sequence 140, App
82	10	9.2	15	2	US-08-553-501A-66	Sequence 66, Appl
83	10	9.2	15	2	US-08-553-501A-70	Sequence 70, Appl
84	10	9.2	15	2	US-08-518-157B-27	Sequence 27, Appl
85	10	9.2	15	2	US-08-560-558B-2	Sequence 2, Appl
86	10	9.2	15	2	US-08-765-783A-88	Sequence 88, Appl
87	10	9.2	15	2	US-08-470-139-11	Sequence 11, Appl
88	10	9.2	15	2	US-08-649-100-26	Sequence 26, Appl
89	10	9.2	15	3	US-09-205-231-66	Sequence 66, Appl
90	10	9.2	15	3	US-09-205-231-70	Sequence 70, Appl
91	10	9.2	15	3	US-08-569-147-38	Sequence 38, Appl
92	10	9.2	15	3	US-09-416-557-88	Sequence 88, Appl
93	10	9.2	15	3	US-09-347-061-11	Sequence 11, Appl
94	10	9.2	15	4	US-09-425-638A-85	Sequence 85, Appl
95	10	9.2	15	4	US-09-543-004-85	Sequence 85, Appl
96	10	9.2	15	4	US-09-543-004-86	Sequence 86, Appl
97	10	9.2	15	4	US-09-217-268A-2	Sequence 2, Appl
98	10	9.2	15	4		
99	10	9.2	15	4		
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ALIGNMENTS

RESULT 1

US-08-488-113B-153
; Sequence 153, Application US/08488113B
; Patent No. 5744580
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studulka, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,113B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 153:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-488-113B-153

Query Match 23.9%; Score 26; DB 1; Length 104;

Best Local Similarity 100.0%; Pred. No. 2.4e-17; Mismatches 0; Indels 0; Gaps 0;

QY 2 SALTGPASVSGSPQSITISCTGTS 27
DB 2 SALTGPASVSGSPQSITISCTGTS 27

RESULT 2

US-08-477-484B-153
; Sequence 153, Application US/08477484B
; Patent No. 5756699
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studulka, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,484B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 153:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-477-484B-153

Query Match 23.9%; Score 26; DB 1; Length 104;

Best Local Similarity 100.0%; Pred. No. 2.4e-17; Mismatches 0; Indels 0; Gaps 0;

QY 2 SALTGPASVSGSPQSITISCTGTS 27
DB 2 SALTGPASVSGSPQSITISCTGTS 27

RESULT 3

US-08-107-669D-17
; Sequence 17, Application US/08107669D
; Patent No. 5766886
; GENERAL INFORMATION:

APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/107,669D
FILING DATE: 13-AUG-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Michele A. Cimbala
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0610.1000001/MAC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/371-2600
TELEFAX: 202/371-2540
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-107-669D-17

Query Match 23.9%; Score 26; DB 1; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.4e-17;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SALTQPASVSGSPGQSITISCTGTSS 27
DB 2 SALTQPASVSGSPGQSITISCTGTSS 27

RESULT 4
US-08-472-788A-17
Sequence 17, Application US/08472788A
Patent No. 5770196
GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,788A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/082,842
FILING DATE: 23-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0610.1000003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/371-2600
TELEFAX: 202/371-2540
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-472-788A-17

Query Match 23.9%; Score 26; DB 1; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.4e-17;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SALTQPASVSGSPGQSITISCTGTSS 27
DB 2 SALTQPASVSGSPGQSITISCTGTSS 27

RESULT 5
US-08-477-531B-17
Sequence 17, Application US/08477531B
Patent No. 5821123
GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,531B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/107,669
FILING DATE: 13-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Michele A. Cimbala
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0610.1000004/MAC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/371-2600

TELEFAX: 202/371-2540
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 104 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-477-531B-17

Query Match 23.9%; Score 26; DB 2; Length 104;
 Best Local Similarity 100.0%; Pred. No. 2.4e-17;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 2 SALTOPASVSGSPGSGITISCTGTS 27
 DB 2 SALTOPASVSGSPGSGITISCTGTS 27

RESULT 6
 US-08-646-360-153
 Sequence 153, Application US/08646360
 Patent No. 5837491
 GENERAL INFORMATION:
 APPLICANT: Better, Marc D.
 APPLICANT: Carroll, Stephen F.
 APPLICANT: Studnicka, Gary M.
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
 TITLE OF INVENTION: Proteins
 NUMBER OF SEQUENCES: 173
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.
 STREET: 500 West Madison Street, 34th floor
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60661
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/646,360
 FILING DATE: 13-MAY-1996
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/05348
 FILING DATE: 12-MAY-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/064,691
 FILING DATE: 12-MAY-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/988,430
 FILING DATE: 09-DEC-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/901,707
 FILING DATE: 19-JUN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/787,567
 FILING DATE: 04-NOV-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: McNicholas, Janet M.
 REGISTRATION NUMBER: 32,918
 REFERENCE/DOCKET NUMBER: 200-70.24
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/707-8889
 TELEFAX: 312/707-9155
 TELEX: 650 388-1248
 INFORMATION FOR SEQ ID NO: 153:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 104 amino acids
 TYPE: amino acid
 STRANDEDNESS: double

TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-646-360-153

Query Match 23.9%; Score 26; DB 2; Length 104;
 Best Local Similarity 100.0%; Pred. No. 2.4e-17;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 2 SALTOPASVSGSPGSGITISCTGTS 27
 DB 2 SALTOPASVSGSPGSGITISCTGTS 27

RESULT 7
 US-08-082-842A-17
 Sequence 17, Application US/08082842A
 Patent No. 5869619
 GENERAL INFORMATION:
 APPLICANT: Studnicka, Gary M.
 TITLE OF INVENTION: Modified Antibody Variable Domains
 NUMBER OF SEQUENCES: 89
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
 STREET: 1100 New York Ave., N.W., Suite 600
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005-3934
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/082,842A
 FILING DATE: 23-JUN-1993
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/10906
 FILING DATE: 14-DEC-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/808,464
 FILING DATE: 13-DEC-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Ciambale, Michele A.
 REGISTRATION NUMBER: 33,851
 REFERENCE/DOCKET NUMBER: 0610.1000002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202/371-2600
 TELEFAX: 202/371-2540
 TELEX:
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 104 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-082-842A-17

Query Match 23.9%; Score 26; DB 2; Length 104;
 Best Local Similarity 100.0%; Pred. No. 2.4e-17;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 2 SALTOPASVSGSPGSGITISCTGTS 27
 DB 2 SALTOPASVSGSPGSGITISCTGTS 27

RESULT 8
 US-08-839-765-153
 Sequence 153, Application US/08839765
 Patent No. 6146631
 GENERAL INFORMATION:

APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 153:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-839-765-153

Query Match 23.9%; Score 26; DB 3; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.4e-17;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SALTQPASVSGSPGOSITISCTGTS 27
DB 2 SALTQPASVSGSPGOSITISCTGTS 27

RESULT 9
US-09-136-389-153
Sequence 153; Application US/09136389
Patent No. 6146850
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.

NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 153:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-136-389-153

Query Match 23.9%; Score 26; DB 3; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.4e-17;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SALTQPASVSGSPGOSITISCTGTS 27
DB 2 SALTQPASVSGSPGOSITISCTGTS 27

RESULT 10
US-09-610-838-153
Sequence 153; Application US/09610838
Patent No. 6376217
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.

STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/610,838
FILING DATE: 06-JUL-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
FILING DATE: 18-AUG-1998
APPLICATION NUMBER: 08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 153:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-610-838-153

Query Match 23.9%; Score 26; DB 4; Length 104;
Best Local Similarity 100.0%; Pred. NO. 2.4e-17;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SALTQPASVSGSPQSITISCTGTS 27
DB 2 SALTQPASVSGSPQSITISCTGTS 27
RESULT 11
US-09-711-485-153
Sequence 153, Application US/09711485
Patent No. 6649742
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnik, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
PROTEINS
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor

CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/711,485
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/839,765
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 153:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-711-485-153

Query Match 23.9%; Score 26; DB 4; Length 104;
Best Local Similarity 100.0%; Pred. NO. 2.4e-17;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SALTQPASVSGSPQSITISCTGTS 27
DB 2 SALTQPASVSGSPQSITISCTGTS 27
RESULT 12
US-08-765-179B-19
Sequence 19, Application US/08765179B
Patent No. 5854027
GENERAL INFORMATION:
APPLICANT: STEIPE, Boris
APPLICANT: STEINBACHER, Stefan
TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY
OF ANTIBODIES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
STREET: 655 Fifteenth Street N.W. Suite 330
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,179B
FILING DATE: 14-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/02626
FILING DATE: 06-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 25 115.7
FILING DATE: 15-JUL-1994
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 64 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-765-179B-19

Query Match 17.4%; Score 19; DB 2; Length 64;
Best Local Similarity 100.0%; Pred. No. 6.8e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 TASLTISGLQAEDEADYYC 90
DB 39 TASLTISGLQAEDEADYYC 57

RESULT 13
US-09-157-370-5
Sequence 5, Application US/09157370A
Patent No. 6262238
GENERAL INFORMATION:
APPLICANT: STEINBACHER, Stefan
TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY OF ANTIBODIES
FILE REFERENCE: PB341-8072
CURRENT APPLICATION NUMBER: US/09/157,370A
EARLIER FILING DATE: 1998-09-21
EARLIER APPLICATION NUMBER: 08/765,179
EARLIER FILING DATE: 1997-01-14
EARLIER APPLICATION NUMBER: PCT/EP95/02626
EARLIER FILING DATE: 1995-07-06
EARLIER APPLICATION NUMBER: DE/P44 25 115.7
EARLIER FILING DATE: 1994-07-15
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
US-09-157-370-5

Query Match 17.4%; Score 19; DB 3; Length 109;
Best Local Similarity 100.0%; Pred. No. 1e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 TASLTISGLQAEDEADYYC 90
DB 69 TASLTISGLQAEDEADYYC 87

RESULT 14
US-09-240-274-69
Sequence 69, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

FILE REFERENCE: 09596-42U2
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 69
LENGTH: 104
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain S01
US-09-240-274-69

Query Match 15.6%; Score 17; DB 3; Length 104;
Best Local Similarity 100.0%; Pred. No. 7.9e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 TASLTISGLQAEDEADYY 88
DB 67 TASLTISGLQAEDEADYY 83

RESULT 15
US-09-240-274-68
Sequence 68, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-42U2
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 68
LENGTH: 108
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain R01
US-09-240-274-68

Query Match 15.6%; Score 17; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. No. 8.2e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 SGLQAEDEADYYCSSFA 94
DB 77 SGLQAEDEADYYCSSFA 93

RESULT 16
US-07-942-245-8
Sequence 8, Application US/07942245
Patent No. 5639641
GENERAL INFORMATION:
APPLICANT: PEDERSEN, Jan T.
APPLICANT: SEARLE, Stephen M. J.
APPLICANT: REES, Anthony R.
APPLICANT: ROGUSKA, Michael A.
APPLICANT: GUILD, Braydon C.
TITLE OF INVENTION: SURFACE RESIDUE VENEERING OF RODENT
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 522

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
;; STREET: 2100 Pennsylvania Avenue, N.W.
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: United States
;; ZIP: 20037-3202
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: HP 9000/700 Workstation
;; OPERATING SYSTEM: UNIX
;; SOFTWARE: In house
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/942,245
;; FILING DATE: 09-SEP-1992
;; CLASSIFICATION: 530
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 293-7060
;; TELEFAX: (202) 293-7860
;; TELEX: 6491103
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 103 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-07-942-245-8

Query Match 11.0%; Score 12; DB 1; Length 103;
Best Local Similarity 100.0%; Pred. No. 0.00043;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 GLOAEDEADYYC 90
DB 71 GLOAEDEADYYC 82

RESULT 17
US-08-107-669D-3
; Sequence 3, Application US/08107669D
; Patent No. 5766886
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/107,669D
; FILING DATE: 13-AUG-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/808,464
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Michele A. Cimbalà
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0610.1000001/MAC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/371-2600

;; TELEFAX: 202/371-2540
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 103 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-107-669D-3

Query Match 11.0%; Score 12; DB 1; Length 103;
Best Local Similarity 100.0%; Pred. No. 0.00043;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 GLOAEDEADYYC 90
DB 72 GLOAEDEADYYC 83

RESULT 18
US-08-472-788A-3
; Sequence 3, Application US/08472788A
; Patent No. 5770196
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,788A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/082,842
; FILING DATE: 23-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/808,464
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbalà, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0610.1000003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/371-2600
; TELEFAX: 202/371-2540
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 103 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-472-788A-3

Query Match 11.0%; Score 12; DB 1; Length 103;
Best Local Similarity 100.0%; Pred. No. 0.00043;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 GLOAEDEADYYC 90
DB 71 GLOAEDEADYYC 82

Db 72 GLOAEDEADYYC 83

RESULT 19

US-08-477-531B-3

Sequence 3, Application US/08477531B

Patent No. 5821123

GENERAL INFORMATION:

APPLICANT: Studnicka, Gary M.

TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)

NUMBER OF SEQUENCES: 67

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.

STREET: 1100 New York Ave., N.W., Suite 600

CITY: Washington

STATE: D.C.

COUNTRY: United States of America

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477,531B

FILING DATE: 07-JUN-1995

CLASSIFICATION: 436

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/107,669

FILING DATE: 13-AUG-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/10906

FILING DATE: 14-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/808,464

FILING DATE: 13-DEC-1991

ATTORNEY/AGENT INFORMATION:

NAME: Michele A. Cimbalà

REGISTRATION NUMBER: 33,851

REFERENCE/DOCKET NUMBER: 0610.1000004/MAC

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202/371-2600

TELEFAX: 202/371-2540

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 103 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-477-531B-3

Query Match 11.0%; Score 12; DB 2; Length 103;

Best Local Similarity 100.0%; Pred. No. 0.00043;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 GLOAEDEADYYC 90

Db 72 GLOAEDEADYYC 83

RESULT 20

US-08-082-842A-3

Sequence 3, Application US/08082842A

Patent No. 5869619

GENERAL INFORMATION:

APPLICANT: Studnicka, Gary M.

TITLE OF INVENTION: Modified Antibody Variable Domains

NUMBER OF SEQUENCES: 89

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.

STREET: 1100 New York Ave., N.W., Suite 600

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/082,842A

FILING DATE: 23-JUN-1993

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/10906

FILING DATE: 14-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/808,464

FILING DATE: 13-DEC-1991

ATTORNEY/AGENT INFORMATION:

NAME: Cimbalà, Michele A.

REGISTRATION NUMBER: 33,851

REFERENCE/DOCKET NUMBER: 0610.1000002

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202/371-2600

TELEFAX: 202/371-2540

TELEX:

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 103 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-082-842A-3

Query Match 11.0%; Score 12; DB 2; Length 103;

Best Local Similarity 100.0%; Pred. No. 0.00043;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 GLOAEDEADYYC 90

Db 72 GLOAEDEADYYC 83

RESULT 21

US-08-992-176-3

Sequence 3, Application US/08992176

Patent No. 6125331

GENERAL INFORMATION:

APPLICANT: TOH, Hiroyuki

TITLE OF INVENTION: STRUCTURAL ALIGNMENT METHOD MAKING USE OF A DOUBLE

FILE REFERENCE: 9200-0001-2

CURRENT APPLICATION NUMBER: US/08/992,176

EARLIER FILING DATE: 1997-12-17

EARLIER APPLICATION NUMBER: JP 8-340727

EARLIER FILING DATE: 1996-12-20

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 3

LENGTH: 103

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:beta-protein

US-08-992-176-3

Query Match 11.0%; Score 12; DB 3; Length 103;

Best Local Similarity 100.0%; Pred. No. 0.00043;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 GLOAEDEADYYC 90

Db 72 GLOAEDEADYYC 83

RESULT 22
US-09-240-274-49
Sequence 49, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-42U2
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/026,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 49
LENGTH: 104
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain J04
US-09-240-274-49

Query Match 11.0%; Score 12; DB 3; Length 104;
Best Local Similarity 100.0%; Pred. No. 0.00043;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 81 QAEADADYCCSS 92
Db 76 QAEADADYCCSS 87

RESULT 23
US-08-765-179B-10
Sequence 10, Application US/08765179B
Patent No. 5854027
GENERAL INFORMATION:
APPLICANT: STEINBACHER, Stefan
TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
STREET: 655 Fifteenth Street N.W. Suite 330
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,179B
FILING DATE: 14-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/02626
FILING DATE: 06-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 25 115.7
FILING DATE: 15-JUL-1994
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 64 amino acids
TYPE: amino acid
STRANDEDNESS:

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-765-179B-10

Query Match 10.1%; Score 11; DB 2; Length 64;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 42 PGKAPKLLIYD 52
Db 9 PGKAPKLLIYD 19

RESULT 24
US-08-851-362D-20
Sequence 20, Application US/08851362D
Patent No. 6235883
GENERAL INFORMATION:
APPLICANT: Jakobovits, Aya
APPLICANT: Yang, Xiao-Dong
APPLICANT: Gallo, Michael
APPLICANT: Jia, Xiao-Chi
TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
FILE REFERENCE: Cell 4.20
CURRENT APPLICATION NUMBER: US/08/851,362D
CURRENT FILING DATE: 1997-05-05
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 20
LENGTH: 76
TYPE: PRT
ORGANISM: human
US-08-851-362D-20

Query Match 10.1%; Score 11; DB 3; Length 76;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 42 PGKAPKLLIYD 52
Db 21 PGKAPKLLIYD 31

RESULT 25
US-08-290-592E-19
Sequence 19, Application US/08290592E
Patent No. 5824307
GENERAL INFORMATION:
APPLICANT: JOHNSON, L.
TITLE OF INVENTION: Human Murine Chimeric Antibodies Against
TITLE OF INVENTION: Respiratory Syncytical Virus
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI, STEWART &
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,592E
FILING DATE: August 15, 1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/813,372
FILING DATE: December 23, 1991

ATTORNEY/AGENT INFORMATION:
 NAME: Olsstein, Elliot M.
 REGISTRATION NUMBER: 24,025
 REFERENCE/DOCKET NUMBER: 469201-257
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-994-1700
 TELEFAX: 201-994-1744
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 95 AMINO ACIDS
 TYPE: AMINO ACID
 TOPOLOGY: LINEAR
 MOLECULE TYPE: PROTEIN
 US-08-290-592E-19

Query Match 10.1%; Score 11; DB 2; Length 95;
 Best Local Similarity 100.0%; Pred. No. 0.0035;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 PGKAPKLLIYD 52
 Db 40 PGKAPKLLIYD 50

Search completed: March 15, 2004, 07:44:32
 Job time : 24 secs

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OM protein - protein search, using sw model

Run on: March 15, 2004, 07:40:14 ; Search time 20 Seconds

(without alignments)
524.244 Million cell updates/sec

Title: US-09-620-955B-4

Perfect score: 109

Sequence: 1 OSALTOPASVSGSPGQSITL.....CSSFANSGLPGGKIVTL 109

Scoring table: OHIGO

Searched: 283366 seqs, 96191526 residues

Word size: 0

Total number of hits satisfying chosen parameters: 44099

Minimum DB seq length: 0

Maximum DB seq length: 109

Post-processing: Listing first 100 summaries

Database:

PIR_78:*
1: pirl:*
2: pirl2:*
3: pirl3:*
4: pirl4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	25.7	99	2	IG lambda chain -
2	28	25.7	99	2	IG lambda chain -
3	20	18.3	99	2	IG lambda chain -
4	19	17.4	99	2	IG lambda chain -
5	19	17.4	109	1	IG lambda chain -
6	12	11.0	99	2	IG lambda chain -
7	12	11.0	99	2	IG lambda chain -
8	12	11.0	99	2	IG lambda chain -
9	12	11.0	103	1	IG lambda chain -
10	11	10.1	87	2	IG kappa chain V r
11	11	10.1	87	2	IG kappa chain V r
12	11	10.1	88	2	IG kappa chain V r
13	11	10.1	88	2	IG kappa chain V r
14	11	10.1	95	2	IG kappa chain V r
15	11	10.1	95	2	IG kappa chain V r
16	11	10.1	107	2	IG kappa chain V r
17	11	10.1	108	1	IG kappa chain V r
18	11	10.1	108	1	IG kappa chain V r
19	11	10.1	53	2	IG lambda chain V r
20	10	9.2	60	2	IG lambda chain V r
21	10	9.2	65	2	IG kappa chain V r
22	10	9.2	82	2	IG kappa chain V r
23	10	9.2	86	2	IG kappa chain V r
24	10	9.2	86	2	IG kappa chain V r
25	10	9.2	87	2	IG kappa chain V r
26	10	9.2	87	2	IG kappa chain V r
27	10	9.2	87	2	IG kappa chain V r
28	10	9.2	88	2	IG kappa chain V r
29	10	9.2	88	2	IG kappa chain V r

30	10	9.2	88	2	S21520	IG kappa chain V r
31	10	9.2	88	2	S21522	IG kappa chain V r
32	10	9.2	88	2	S34104	IG kappa chain V r
33	10	9.2	92	2	A27633	IG lambda-2 chain
34	10	9.2	96	2	S36060	IG lambda chain -
35	10	9.2	98	2	S36046	IG lambda chain -
36	10	9.2	98	2	S41813	IG kappa chain V r
37	10	9.2	99	2	S36059	IG lambda chain -
38	10	9.2	103	2	A38923	AL type amyloid fi
39	10	9.2	103	2	S18731	IG kappa chain V-J
40	10	9.2	105	2	S49533	anti-Sm antibody V
41	10	9.2	106	2	S38495	IG lambda chain -
42	10	9.2	106	2	S40091	IG light chain - m
43	10	9.2	106	2	PC2397	anti-retanus toxin
44	10	9.2	107	1	L4H0HL	IG lambda chain V-
45	10	9.2	107	2	S36264	IG lambda chain V
46	10	9.2	107	2	S36262	IG lambda chain V
47	10	9.2	107	2	S36269	IG lambda chain V
48	10	9.2	108	1	KIHURE	IG kappa chain V-I
49	10	9.2	108	1	KIHOKA	IG kappa chain V-I
50	10	9.2	108	1	KVMS09	IG kappa chain V r
51	10	9.2	108	1	KVMS09	IG kappa chain V r
52	10	9.2	108	1	KVMS06	IG kappa chain V r
53	10	9.2	108	1	KVMS82	IG kappa chain V r
54	10	9.2	108	1	L3H0SH	IG lambda chain V-
55	10	9.2	108	2	S38498	IG lambda chain -
56	10	9.2	108	2	S47184	IG lambda chain -
57	10	9.2	108	2	S19674	IG kappa chain V r
58	10	9.2	108	2	S31977	IG kappa chain - h
59	10	9.2	108	2	B49047	IG kappa chain V r
60	10	9.2	108	2	S47182	IG kappa chain - h
61	10	9.2	108	2	S36277	IG lambda chain V
62	10	9.2	108	2	S36279	IG lambda chain V
63	10	9.2	109	2	S38496	IG lambda chain -
64	10	9.2	109	2	S19663	IG lambda chain V
65	10	9.2	109	2	S68171	IG lambda chain -
66	10	9.2	109	2	S31998	IG kappa chain - h
67	9	8.3	108	1	KIHUWS	IG kappa chain V-I
68	9	8.3	108	2	S44122	IG kappa chain V r
69	9	8.3	109	1	KIHUMV	IG kappa chain V-I
70	9	8.3	109	1	S31981	IG kappa chain - h
71	9	8.3	109	2	S31978	IG kappa chain - h
72	9	8.3	109	2	S38494	IG lambda chain -
73	9	8.3	109	2	JN0296	IG kappa chain V-J
74	8	7.3	57	2	PH0879	IG kappa chain V r
75	8	7.3	90	2	S24218	IG kappa chain - m
76	8	7.3	94	2	C32529	IG lambda chain V
77	8	7.3	95	2	S49571	IG lambda chain pr
78	8	7.3	97	2	I51216	IG light chain var
79	8	7.3	98	2	S36068	IG lambda chain -
80	8	7.3	98	2	S36047	IG lambda chain -
81	8	7.3	98	2	S36048	IG lambda chain -
82	8	7.3	98	2	S36050	IG lambda chain -
83	8	7.3	99	2	S36054	IG lambda chain -
84	8	7.3	108	1	KIHUKU	IG kappa chain V-I
85	8	7.3	108	1	KIHUKU	IG kappa chain V-I
86	8	7.3	109	1	L1HURP	IG lambda chain V-
87	8	7.3	109	1	L1HURP	IG lambda chain V-
88	7	6.4	13	2	S03063	IG lambda chain J
89	7	6.4	39	2	G32529	IG lambda chain V
90	7	6.4	47	2	E32529	IG lambda chain V
91	7	6.4	75	2	S40337	IG kappa chain V-J
92	7	6.4	77	2	D30502	IG kappa chain V r
93	7	6.4	91	2	PH1071	IG light chain V r
94	7	6.4	94	2	S37525	IG kappa chain V r
95	7	6.4	92	2	S37523	IG kappa chain V r
96	7	6.4	92	2	S37535	IG kappa chain V r
97	7	6.4	92	2	S37510	IG kappa chain V r
98	7	6.4	92	2	S37532	IG kappa chain V r
99	7	6.4	94	2	A01955	IG kappa chain V r
100	7	6.4	95	2	S36065	IG lambda chain -

ALIGNMENTS

RESULT 1

S36055

Ig lambda chain - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000

C/Accession: S36055

R/Williams, S.C.

A:Reference number: S36046

A:Accession: S36055

A/Status: Preliminary

A/Molecule type: DNA

A/Residues: 1-99 <WIL>

A/Cross-references: EMBL:Z22196; NID:G312856; PIDN:CA80206.1; PID:G312857

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-92/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 100.0%; Score 28; DB 2; Length 99;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSALTQPAVSQSPGQSIITISCTGTSSD 28

DB 1 QSALTQPAVSQSPGQSIITISCTGTSSD 28

RESULT 2

S36056

Ig lambda chain - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000

C/Accession: S36056

R/Williams, S.C.

A:Reference number: S36046

A:Accession: S36056

A/Status: Preliminary

A/Molecule type: DNA

A/Residues: 1-99 <WIL>

A/Cross-references: EMBL:Z22197; NID:G312317; PIDN:CA80207.1; PID:G312318

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-92/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 100.0%; Score 28; DB 2; Length 99;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSALTQPAVSQSPGQSIITISCTGTSSD 28

DB 1 QSALTQPAVSQSPGQSIITISCTGTSSD 28

RESULT 3

S36058

Ig lambda chain - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 23-Jul-1999

C/Accession: S36058

R/Williams, S.C.

A:Reference number: S36046

A:Accession: S36058

A/Status: Preliminary

A/Molecule type: DNA

A/Residues: 1-99 <WIL>

A/Cross-references: EMBL:Z22199; NID:G312858; PIDN:CA80209.1; PID:G312859

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

Query Match

Best Local Similarity 18.3%; Score 20; DB 2; Length 99;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 TASLTISGLQAEADADYYC 91

DB 72 TASLTISGLQAEADADYYC 91

RESULT 4

S36057

Ig lambda chain - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000

C/Accession: S36057

R/Williams, S.C.

A:Reference number: S36046

A:Accession: S36057

A/Status: Preliminary

A/Molecule type: DNA

A/Residues: 1-99 <WIL>

A/Cross-references: EMBL:Z22198; NID:G312319; PIDN:CA80208.1; PID:G312320

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-92/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 17.4%; Score 19; DB 2; Length 99;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 TASLTISGLQAEADADYYC 90

DB 72 TASLTISGLQAEADADYYC 90

RESULT 5

L2HUBR

Ig lambda chain V-II region (Bur) - human

C/Species: Homo sapiens (man)

C/Date: 31-Mar-1980 #sequence_revision 31-Mar-1980 #text_change 02-Sep-1997

C/Accession: A01974

R/Infante, A.J.; Putnam, F.W.

J. Biol. Chem. 254, 9006-9016, 1979

A/Title: Primary structure of a human IgA1 immunoglobulin. V. Amino acid sequence of

A/Reference number: A01974; MUID:8006606; PMID:113407

A/Accession: A01974

A/Molecule type: protein

A/Residues: 1-109 <IMF>

A/Note: Cys-91 appears to be a free but unreactive sulfhydryl group

A/Note: the C region of this chain has the Kern+ and Meg+ markers

C/Comment: This chain was isolated from a myeloma protein.

C/Genetics:

A/Gene: GDB:IGLV9

A/Cross-references: GDB:119342; OMIM:147240

A/Map position: 22q11.2-22q11.2

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light

chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate int

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin; pyroglytamic acid

F/15-92/Domain: immunoglobulin homology <IMM>

F/1/Modified site: pyrolysine carboxylic acid (Gln) #status experimental

Query Match

Best Local Similarity 17.4%; Score 19; DB 1; Length 109;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 TASLTISGLQAEADADYYC 90

DB 72 TASLTISGLQAEADADYYC 90

RESULT 6

IG lambda chain - human (fragment)
S36051
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
C:Accession: S36051
R:Williams, S.C.
Submitted to the EMBL Data Library, April 1993
A:Reference number: S36046
A:Accession: S36051
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-99 <WIL>
A:Cross-references: EMBL:Z22192; NID:G312305; PIDN:CAA80202.1; PID:G312306
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-92/Domain: immunoglobulin homology <IMM>

Query Match 11.0%; Score 12; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 79 GLQAEDEADYYC 90
DB 79 GLQAEDEADYYC 90

RESULT 7

IG lambda chain - human (fragment)
S36052
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
C:Accession: S36052
R:Williams, S.C.
Submitted to the EMBL Data Library, April 1993
A:Reference number: S36046
A:Accession: S36052
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-99 <WIL>
A:Cross-references: EMBL:Z22193; NID:G312307; PIDN:CAA80203.1; PID:G312308
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-92/Domain: immunoglobulin homology <IMM>

Query Match 11.0%; Score 12; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 79 GLQAEDEADYYC 90
DB 79 GLQAEDEADYYC 90

RESULT 8

IG lambda chain - human (fragment)
S36053
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
C:Accession: S36053
R:Williams, S.C.
Submitted to the EMBL Data Library, April 1993
A:Reference number: S36046
A:Accession: S36053
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-99 <WIL>
A:Cross-references: EMBL:Z22194; NID:G312315; PIDN:CAA80204.1; PID:G312316
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-92/Domain: immunoglobulin homology <IMM>

Query Match 11.0%; Score 12; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 79 GLQAEDEADYYC 90
DB 79 GLQAEDEADYYC 90

RESULT 9

IG lambda chain V-I region (Newm) - human (tentative sequence)
L1HUNM
C:Species: Homo sapiens (man)
C:Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 31-Mar-2000
C:Accession: A01968
R:Chen, B.L.; Poljak, R.J.
Biochemistry 13, 1295-1302, 1974
A:Title: Amino acid sequence of the (lambda) light chain of a human myeloma immunoglobulin
A:Reference number: A03375; MUID:74109253; PMID:4814727
A:Accession: A01968
A:Molecule type: protein
A:Residues: 1-103 <CHB>
A>Note: the absence of seven residues found in other lambda chains was confirmed by
A>Note: the C region of this chain has the Oz+ marker
R:Saul, F.A.; Amzel, L.M.; Poljak, R.J.
J. Biol. Chem. 253, 585-597, 1978
A:Title: Preliminary refinement and structural analysis of the Fab fragment from human myeloma protein
A:Reference number: A92235; MUID:78066916; PMID:618887
A:Contents: annotation; X-ray crystallography; 2.0 angstroms
A>Note: the structure of the Fab fragment of the IgG1 myeloma protein Newm was determined
C:Genetics:
A:Gene: GDB:IGLV@
A:Cross-references: GDB:119342; OMIM:147240
A:Map position: 22q11.2-22q11.2
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into higher order structures.
C:Keywords: blocked amino end; heterotetramer
F:15-85/Domain: immunoglobulin homology <IMM>
F:1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #s1
F:22-83/Disulfide bonds: #status predicted

Query Match 11.0%; Score 12; DB 1; Length 103;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 79 GLQAEDEADYYC 90
DB 72 GLQAEDEADYYC 83

RESULT 10

IG kappa chain V region (018) - human
S42265
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-1999
C:Accession: S42265
R:Scott, M.G.; Crimmins, D.L.; McCourt, D.W.; Chung, G.; Schaeble, K.F.; Thibe, R.; J. Immunol. 147, 4007-4013, 1991
A:Title: Clonal characterization of the human IgG antibody repertoire to Haemophilus influenzae type b
A:Reference number: S42263; MUID:92043792; PMID:1940382
A:Accession: S42265
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-62 <SCO>
A:Cross-references: EMBL:M64856
C:Genetics:
A:Intons: 19/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 10.1%; Score 11; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 0.00071;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 PGKAPKLLIYD 52
 |||||
 DB 40 PGKAPKLLIYD 50

RESULT 11

152592

Ig kappa chain V region - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000

C/Accession: I52592

R/Wagner, S.D.; Martineili, V.; Luzzatto, L.

B/Exp. Med. 174, 1639-1652, 1991

A/Title: Similar patterns of V kappa gene usage but different degrees of somatic mutation

A/Reference number: I52592; MUID:94264318; PMID:8204889

A/Accession: I52592

A/Status: preliminary; translated from GB/EMBL/DBD

A/Molecule type: DNA

A/Residues: 1-87 <RES>

A/Cross-references: GB:S71057; NID:G547053; PIDN:AB30971.1; PID:G547054

C/Genetics:

A/Gene: IGKV

C/Superfamily: immunoglobulin V region; immunoglobulin homology

F/9-83/Domain: immunoglobulin homology <IMM>

Query Match 10.1%; Score 11; DB 2; Length 87;
 Best Local Similarity 100.0%; Pred. No. 0.00095;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 PGKAPKLLIYD 52
 |||||
 DB 33 PGKAPKLLIYD 43

RESULT 12

S34088

Ig kappa chain V region - human

C/Species: Homo sapiens (man)

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000

C/Accession: S34088

R/Wagner, S.D.; Luzzatto, L.

B/Exp. Immunol. 23, 391-397, 1993

A/Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed

A/Reference number: S34076; MUID:93170387; PMID:8436174

A/Accession: S34088

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-86 <MAG>

A/Cross-references: EMBL:X67172

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/9-83/Domain: immunoglobulin homology <IMM>

Query Match 10.1%; Score 11; DB 2; Length 88;
 Best Local Similarity 100.0%; Pred. No. 0.00095;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 PGKAPKLLIYD 52
 |||||
 DB 33 PGKAPKLLIYD 43

RESULT 13

S34087

Ig kappa chain V region - human

C/Species: Homo sapiens (man)

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000

C/Accession: S34087

R/Wagner, S.D.; Luzzatto, L.

B/Exp. Immunol. 23, 391-397, 1993

A/Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed

A/Reference number: S34076; MUID:93170387; PMID:8436174

A/Accession: S34087

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-88 <MAG>

A/Cross-references: EMBL:X67171

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/9-83/Domain: immunoglobulin homology <IMM>

Query Match 10.1%; Score 11; DB 2; Length 88;
 Best Local Similarity 100.0%; Pred. No. 0.00095;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 PGKAPKLLIYD 52
 |||||
 DB 33 PGKAPKLLIYD 43

RESULT 14

PH0862

Ig kappa chain V region (anti-DNA, III-3R) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jan-2000

C/Accession: PH0862

R/Mahleimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, E

J. Exp. Med. 174, 1639-1652, 1991

A/Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idic

A/Reference number: PH0862; MUID:92078875; PMID:1660528

A/Accession: PH0862

A/Molecule type: DNA

C/Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that b

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/1-23/Region: framework 1

F/16-50/Domain: immunoglobulin homology <IMM>

F/24-34/Region: complementarity-determining 1

F/35-49/Region: framework 2

F/50-56/Region: complementarity-determining 2

F/57-88/Region: framework 3

F/89-95/Region: complementarity-determining 3

Query Match 10.1%; Score 11; DB 2; Length 95;
 Best Local Similarity 100.0%; Pred. No. 0.001;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 PGKAPKLLIYD 52
 |||||
 DB 40 PGKAPKLLIYD 50

RESULT 15

PH0864

Ig kappa chain V region (anti-DNA, IC4) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jan-2000

C/Accession: PH0864

R/Mahleimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, E

J. Exp. Med. 174, 1639-1652, 1991

A/Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idic

A/Reference number: PH0862; MUID:92078875; PMID:1660528

A/Accession: PH0864

A/Molecule type: DNA

C/Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that b

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/1-23/Region: framework 1

F/16-50/Domain: immunoglobulin homology <IMM>

F/24-34/Region: complementarity-determining 1

F/35-49/Region: framework 2

F/50-56/Region: complementarity-determining 2

F:57-88/Region: framework 3
F:89-95/Region: complementarity-determining 3

Query Match 10.1%; Score 11; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 PGKAPKLLIYD 52
|||||
DB 40 PGKAPKLLIYD 50

RESULT 16

B46516
Ig lambda chain V region - horse (fragment)
C:Species: Equus caballus (domestic horse)
C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: B46516
R:Home, W.A.; Ford, J.E.; Galsbol, D.M.
J. Immunol. 149, 3927-3936, 1992
A:Title: L chain isotype regulation in horse. I. Characterization of Ig lambda genes.
A:Reference number: A46516; MUID:93094587; PMID:1460283
A:Accession: B46516
A:Status: Preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-107 <HOM>
A:Experimental source: spleen
A:Note: sequence extracted from NCBI backbone (NCBI:P120369)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:23-101/Domain: immunoglobulin homology <IMM>

Query Match 10.1%; Score 11; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 QAEDEADYYCS 91
|||||
DB 90 QAEDEADYYCS 100

RESULT 17

KIHUAV
Ig kappa chain V-I region (Au) - human
C:Species: Homo sapiens (man)
C:Date: 24-Apr-1994 #sequence_revision 02-Jul-1998 #text_change 21-Jan-2000
C:Accession: A91653; A01862; S02573
R:Schlecht, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 353, 345-370, 1972
A:Title: Die Primerstruktur ether monoklonalen Immunglobulin-L-Kette vom kappa-Typ. Sub
A:Reference number: A91653; MUID:72189444; PMID:5028201
A:Accession: A91653
A:Molecule type: protein
A:Residues: 1-108 <SCH>
A:Note: the C region of this chain has the Inv (3) marker

R:Rehlander, H.; Schiffer, M.; Epp, O.; Colman, P.M.; Lattman, E.E.; Schwager, P.; Stei
Biophys. Struct. Mech. 1, 139-146, 1975
A:Title: The structure determination of the variable portion of the Bence-Jones protein
A:Reference number: A90729; MUID:77022433; PMID:1234024
A:Contents: annotation; X-ray crystallography
A:Note: the structure of the V region was determined by molecular replacement methods us
R:Steiner, V.; Chang, J.Y.
FEBS Lett. 222, 6-10, 1987

A:Title: Chemical modification of the carboxyl groups of protein substrates enhances the
A:Reference number: S02572; MUID:88005152; PMID:3115831
A:Contents: annotation
C:Comment: This is a Bence Jones protein.

C:Genetics:
A:Gene: GDB:IGKV1
A:Cross-references: GDB:136264
A:Map position: 2p12-2p12
C:Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate into 18
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>
F:23-88/Disulfide bonds: #status predicted

Query Match 10.1%; Score 11; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 PGKAPKLLIYD 52
|||||
DB 40 PGKAPKLLIYD 50

RESULT 18

KIHUAV
Ig kappa chain V-I region (Roy) - human (tentative sequence)
C:Species: Homo sapiens (man)
C:Date: 24-Apr-1994 #sequence_revision 02-Jul-1998 #text_change 31-Mar-2000
C:Accession: A91638; B94417; A01874; S02575
R:Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 348, 1077-1080, 1967
A:Title: Die chemische Struktur von zwei Bence-Jones-Proteinen (Roy und Cum.) vom kappa
A:Reference number: A91638; MUID:68362076; PMID:5595110
A:Accession: A91638
A:Molecule type: protein
A:Residues: 1-38; GPK, 42-108 <HIL>
A:Note: the sequence of the C region, which has the Inv (1,2) marker, is also given
R:Hilschmann, N.; Barrikot, H.U.; Haes, M.; Langer, B.; Ponstingl, H.; Steinmetz-Kay
in Gamma Globulins: Structure and Function, Franek, F., and Shugar, D., eds., pp.57-

A:Reference number: A94417
A:Reference number: A94417
A:Contents: revisions to residues 39 and 41
A:Accession: B94417
A:Molecule type: protein
A:Residues: 39-41 <HIL2>
R:Steiner, V.; Chang, J.Y.
FEBS Lett. 222, 6-10, 1987

A:Title: Chemical modification of the carboxyl groups of protein substrates enhances
A:Reference number: S02572; MUID:88005152; PMID:3115831
A:Contents: annotation
C:Comment: This is a Bence Jones protein.

C:Genetics:
A:Gene: GDB:IGKV1
A:Cross-references: GDB:136264
A:Map position: 2p12-2p12
C:Complex: an immunoglobulin heterotetramer subunit consists of two identical light chain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate into
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>
F:23-88/Disulfide bonds: #status predicted

Query Match 10.1%; Score 11; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 PGKAPKLLIYD 52
|||||
DB 40 PGKAPKLLIYD 50

RESULT 19

PH0881
Ig kappa chain V region (GOU) - human (fragment)
N:Alternate names: myeloma protein
C:Species: Homo sapiens (man)
C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 09-May-1997
C:Accession: PH0881

R:Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghosein, C.; Smith, A.; Diamond, B.
J. Exp. Med. 174, 1639-1652, 1991
A:Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiot
A:Reference number: PH0881; MUID:92078875; PMID:1660528
A:Accession: PH0881
A:Molecule type: protein

A:Residues: 1-53 <MAN>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-23/Region: framework 1
 F:24-34/Region: complementarity-determining 1
 F:35-49/Region: framework 2
 F:50-53/Region: complementarity-determining 2

Query Match 9.2%; Score 10; DB 2; Length 53;
 Best Local Similarity 100.0%; Pred. No. 0.0065;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 PGKAPKLLIY 51
 |||||
 DB 40 PGKAPKLLIY 49

RESULT 20

A24626
 Ig lambda chain V-II region (Har) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 28-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 16-Aug-1996
 C:Accession: A24626
 R:Bultz, M.; Linke, R.
 Biol. Chem. Hoppe-Seyler 366, 907-915, 1985
 A:Title: Amyloid fibrils derived from V-region together with C-region fragments from a
 A:Reference number: A24626; MUID:86077295; PMID:3335132
 A:Accession: A24626
 A:Molecule type: protein
 A:Residues: 1-60 <EUL>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 9.2%; Score 10; DB 2; Length 60;
 Best Local Similarity 100.0%; Pred. No. 0.0072;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 ASVSGSPGQS 17
 |||||
 DB 1 ASVSGSPGQS 10

RESULT 21

PH0880
 Ig kappa chain V region (SCH) - human (fragment)
 N:Alternate names: myeloma protein
 C:Species: Homo sapiens (man)
 C>Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 09-May-1997
 C:Accession: PH0880
 R:Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.
 J. Exp. Med. 174, 1639-1652, 1991
 A:Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idioType
 A:Reference number: PH0862; MUID:92078875; PMID:160528
 A:Accession: PH0880
 A:Molecule type: protein
 A:Residues: 1-65 <MAN>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-23/Region: framework 1
 F:24-34/Region: complementarity-determining 1
 F:35-49/Region: framework 2
 F:50-56/Region: complementarity-determining 2
 F:57-65/Region: framework 3

Query Match 9.2%; Score 10; DB 2; Length 65;
 Best Local Similarity 100.0%; Pred. No. 0.0077;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 PGKAPKLLIY 51
 |||||
 DB 40 PGKAPKLLIY 49

RESULT 22

S34090
 Ig kappa chain V region - human
 C:Species: Homo sapiens (man)
 C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
 C:Accession: S34090
 R:Wagner, S.D.; Luzzatto, L.
 Eur. J. Immunol. 23, 391-397, 1993
 A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distri
 A:Reference number: S34076; MUID:91170387; PMID:8436174
 A:Accession: S34090
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-82 <WAG>
 A:Cross-references: EMBL:X67174
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:7-81/Domain: immunoglobulin homology <IMV>

Query Match 9.2%; Score 10; DB 2; Length 82;
 Best Local Similarity 100.0%; Pred. No. 0.0093;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 PGKAPKLLIY 51
 |||||
 DB 31 PGKAPKLLIY 40

RESULT 23

S34086
 Ig kappa chain V region - human
 C:Species: Homo sapiens (man)
 C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
 C:Accession: S34086
 R:Wagner, S.D.; Luzzatto, L.
 Eur. J. Immunol. 23, 391-397, 1993
 A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distri
 A:Reference number: S34076; MUID:91170387; PMID:8436174
 A:Accession: S34086
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-86 <WAG>
 A:Cross-references: EMBL:X67169
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:9-83/Domain: immunoglobulin homology <IMV>

Query Match 9.2%; Score 10; DB 2; Length 86;
 Best Local Similarity 100.0%; Pred. No. 0.0097;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 PGKAPKLLIY 51
 |||||
 DB 33 PGKAPKLLIY 42

RESULT 24

S16840
 Ig kappa chain V region - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
 C:Accession: S16840
 R:Blalston, G.; Kuntz, J.L.; Pasquali, J.L.
 Eur. J. Immunol. 21, 1221-1227, 1991
 A:Title: Molecular analysis of V(kappa)IIIT variable regions of polyclonal rheumatoid
 A:Reference number: S16823; MUID:91243737; PMID:1903706
 A:Accession: S16840
 A:Status: preliminary; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-86 <BLA>
 A:Cross-references: EMBL:X54838
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

F:7-81/Domain: immunoglobulin homology <IMM>

Query Match 9.2%; Score 10; DB 2; Length 86;
 Best Local Similarity 100.0%; Pred. No. 0.0097;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 PGKAPKLLIY 51
 |||||
 Db 31 PGKAPKLLIY 40

RESULT 25

S21523
 Ig kappa chain V region - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 20-Feb-1995 #sequence_revision 25-Oct-1996 #text_change 21-Jan-2000
 C/Accession: S34079; S21523
 R/Magner, S.D.; Luzzatto, L.
 Eur. J. Immunol. 23, 391-397, 1993
 A/Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
 A/Reference number: S34076; WUID:93170387; PMID:8436174
 A/Accession: S34079
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-87 <MA2>
 A/Cross-references: EMBL:X66039; NID:G33312; PID:CAA46838.1; PID:G33313
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F:9-83/Domain: immunoglobulin homology <IMM>

Query Match 9.2%; Score 10; DB 2; Length 87;
 Best Local Similarity 100.0%; Pred. No. 0.0098;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 PGKAPKLLIY 51
 |||||
 Db 33 PGKAPKLLIY 42

Search completed: March 15, 2004, 07:43:56
 Job time : 21 secs

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OM protein - protein search, using sw model

Run on: March 15, 2004, 07:42:10 ; Search time 34 Seconds
(without alignments)

676.933 Million cell updates/sec

Title: US-09-620-955b-4

Perfect score: 109

Sequence: 1 OSALTQPAVSSGSPGQSIRI.....CSSFANSGLPGGKXTVTL 109

Scoring table: OLIGO

Searched: Gapop 60.0 , Gapext 60.0

Word size : 0

Total number of hits satisfying chosen parameters: 332758

Minimum DB seq length: 0

Maximum DB seq length: 109

Post-processing: Listing first 100 summaries

Database :

Published Applications AA.*
1: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	25.7	90	14	US-10-125-667-27
2	28	25.7	99	15	US-10-308-817-99
3	28	25.7	99	15	US-10-308-817-101
4	26	23.9	104	14	US-10-127-890-153
5	26	23.9	104	15	US-10-340-189-17
6	26	23.9	104	15	US-10-325-696-17
7	23	21.1	103	14	US-10-026-925-98
8	22	20.2	22	10	US-09-563-222-94
9	21	19.3	50	9	US-09-863-693-14
10	21	19.3	50	9	US-09-863-693-15
11	21	19.3	50	9	US-09-863-693-16
12	21	19.3	50	9	US-09-863-693-17
13	21	19.3	50	9	US-09-863-693-18
14	21	19.3	50	9	US-09-863-693-19
15	21	19.3	50	9	US-09-863-693-20

16	21	19.3	50	9	US-09-863-693-21	Sequence 21, Appl
17	21	19.3	50	9	US-09-863-693-22	Sequence 22, Appl
18	21	19.3	50	11	US-09-373-403-14	Sequence 14, Appl
19	21	19.3	50	11	US-09-373-403-15	Sequence 15, Appl
20	21	19.3	50	11	US-09-373-403-16	Sequence 16, Appl
21	21	19.3	50	11	US-09-373-403-17	Sequence 17, Appl
22	21	19.3	50	11	US-09-373-403-18	Sequence 18, Appl
23	21	19.3	50	11	US-09-373-403-19	Sequence 19, Appl
24	21	19.3	50	11	US-09-373-403-20	Sequence 20, Appl
25	21	19.3	50	11	US-09-373-403-21	Sequence 21, Appl
26	21	19.3	50	11	US-09-373-403-22	Sequence 22, Appl
27	21	19.3	50	14	US-10-143-437-14	Sequence 14, Appl
28	21	19.3	50	14	US-10-143-437-15	Sequence 15, Appl
29	21	19.3	50	14	US-10-143-437-16	Sequence 16, Appl
30	21	19.3	50	14	US-10-143-437-17	Sequence 17, Appl
31	21	19.3	50	14	US-10-143-437-18	Sequence 18, Appl
32	21	19.3	50	14	US-10-143-437-19	Sequence 19, Appl
33	21	19.3	50	14	US-10-143-437-20	Sequence 20, Appl
34	21	19.3	50	14	US-10-143-437-21	Sequence 21, Appl
35	21	19.3	50	14	US-10-143-437-22	Sequence 22, Appl
36	21	19.3	92	9	US-09-925-299-1047	Sequence 1047, Ap
37	21	19.3	92	10	US-09-925-299-1047	Sequence 1047, Ap
38	21	19.3	97	9	US-09-864-761-39459	Sequence 39459, A
39	20	18.3	99	15	US-10-308-817-100	Sequence 100, App
40	20	18.3	107	10	US-09-913-238-67	Sequence 67, Appl
41	19	17.4	32	10	US-09-563-222-96	Sequence 96, Appl
42	19	17.4	99	15	US-10-308-817-98	Sequence 98, Appl
43	19	17.4	103	10	US-09-913-238-3	Sequence 3, Appl
44	17	15.6	104	10	US-09-848-798-69	Sequence 69, Appl
45	17	15.6	108	10	US-09-848-798-68	Sequence 68, Appl
46	15	13.8	99	15	US-10-308-817-97	Sequence 97, Appl
47	12	11.0	82	14	US-10-105-545-32	Sequence 32, Appl
48	12	11.0	97	15	US-10-264-045-4296	Sequence 4296, Ap
49	12	11.0	99	15	US-10-308-817-93	Sequence 93, Appl
50	12	11.0	103	15	US-10-340-189-3	Sequence 3, Appl
51	12	11.0	103	15	US-10-325-696-3	Sequence 3, Appl
52	12	11.0	104	10	US-09-848-798-49	Sequence 49, Appl
53	12	11.0	107	10	US-09-913-238-68	Sequence 68, Appl
54	11	10.1	75	14	US-10-078-958-25	Sequence 25, Appl
55	11	10.1	76	14	US-09-187-693-36	Sequence 36, Appl
56	11	10.1	76	14	US-10-078-958-10	Sequence 10, Appl
57	11	10.1	88	9	US-09-905-243-31	Sequence 31, Appl
58	11	10.1	90	9	US-09-864-761-34739	Sequence 34739, A
59	11	10.1	95	9	US-09-158-120A-19	Sequence 19, Appl
60	11	10.1	95	14	US-10-194-975-56	Sequence 56, Appl
61	11	10.1	95	14	US-10-194-975-57	Sequence 57, Appl
62	11	10.1	95	14	US-10-194-975-63	Sequence 63, Appl
63	11	10.1	95	14	US-10-194-975-64	Sequence 64, Appl
64	11	10.1	95	14	US-10-194-975-72	Sequence 72, Appl
65	11	10.1	95	15	US-10-308-817-3	Sequence 3, Appl
66	11	10.1	95	15	US-10-308-817-4	Sequence 4, Appl
67	11	10.1	95	15	US-10-308-817-10	Sequence 10, Appl
68	11	10.1	95	15	US-10-308-817-11	Sequence 11, Appl
69	11	10.1	95	15	US-10-308-817-19	Sequence 19, Appl
70	11	10.1	95	15	US-10-127-890-158	Sequence 158, App
71	11	10.1	96	15	US-10-340-189-22	Sequence 22, Appl
72	11	10.1	96	15	US-10-325-696-22	Sequence 22, Appl
73	11	10.1	104	14	US-10-078-958-28	Sequence 28, Appl
74	11	10.1	105	9	US-09-187-693-44	Sequence 44, Appl
75	11	10.1	105	9	US-09-187-693-54	Sequence 54, Appl
76	11	10.1	105	9	US-09-187-693-54	Sequence 54, Appl
77	11	10.1	106	9	US-09-796-848-11	Sequence 11, Appl
78	11	10.1	106	9	US-09-796-848-3	Sequence 3, Appl
79	11	10.1	106	9	US-09-796-848-35	Sequence 35, Appl
80	11	10.1	106	9	US-09-771-415-1	Sequence 1, Appl
81	11	10.1	106	9	US-09-771-415-17	Sequence 17, Appl
82	11	10.1	106	9	US-09-771-415-19	Sequence 19, Appl
83	11	10.1	106	9	US-09-771-415-21	Sequence 21, Appl
84	11	10.1	106	9	US-09-771-415-23	Sequence 23, Appl
85	11	10.1	106	9	US-09-771-415-25	Sequence 25, Appl
86	11	10.1	106	9	US-09-996-288-8	Sequence 8, Appl
87	11	10.1	106	9	US-09-996-288-11	Sequence 11, Appl
88	11	10.1	106	9	US-09-996-288-13	Sequence 13, Appl

89 11 10.1 106 9 US-09-996-288-21 Sequence 21, Appl
90 11 10.1 106 9 US-09-996-288-26 Sequence 26, Appl
91 11 10.1 106 9 US-09-996-288-30 Sequence 30, Appl
92 11 10.1 106 9 US-09-996-288-34 Sequence 34, Appl
93 11 10.1 106 9 US-09-996-288-38 Sequence 38, Appl
94 11 10.1 106 9 US-09-996-288-42 Sequence 42, Appl
95 11 10.1 106 9 US-09-996-288-46 Sequence 46, Appl
96 11 10.1 106 9 US-09-996-288-49 Sequence 49, Appl
97 11 10.1 106 9 US-09-996-288-52 Sequence 52, Appl
98 11 10.1 106 9 US-09-996-288-54 Sequence 54, Appl
99 11 10.1 106 9 US-09-996-288-56 Sequence 56, Appl
100 11 10.1 106 9 US-09-996-288-57 Sequence 57, Appl

ALIGNMENTS

RESULT 1
US-10-125-687-27
; Sequence 27, Application US/10125687
; Publication No. US20030054407A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peter
; TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
; FILE REFERENCE: 26050-705
; CURRENT APPLICATION NUMBER: US/10/125,687
; CURRENT FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-125-687-27

Query Match 25.7% Score 28; DB 14; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.2e-19;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSALTQPAVSQSGSPQGSITISCTGTSSD 28
DB 1 QSALTQPAVSQSGSPQGSITISCTGTSSD 28

RESULT 2
US-10-308-817-99
; Sequence 99, Application US/10308817
; Publication No. US2003021861A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; APPLICANT: Wu, Dayang
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 1087-37
; CURRENT APPLICATION NUMBER: US/10/308,817
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 99
; LENGTH: 99
; TYPE: PRT
; ORGANISM: human
US-10-308-817-99

Query Match 25.7% Score 28; DB 15; Length 99;
Best Local Similarity 100.0%; Pred. No. 2.4e-19;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSALTQPAVSQSGSPQGSITISCTGTSSD 28
DB 1 QSALTQPAVSQSGSPQGSITISCTGTSSD 28

RESULT 3

US-10-308-817-101
; Sequence 101, Application US/10308817
; Publication No. US2003021861A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; APPLICANT: Wu, Dayang
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 1087-37
; CURRENT APPLICATION NUMBER: US/10/308,817
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 101
; LENGTH: 99
; TYPE: PRT
; ORGANISM: human
US-10-308-817-101

Query Match 25.7% Score 28; DB 15; Length 99;
Best Local Similarity 100.0%; Pred. No. 2.4e-19;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSALTQPAVSQSGSPQGSITISCTGTSSD 28
DB 1 QSALTQPAVSQSGSPQGSITISCTGTSSD 28

RESULT 4
US-10-127-890-153
; Sequence 153, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnicka, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/127,890
; FILING DATE: 23-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-May-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-May-1994
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-May-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-Dec-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-Jun-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-Nov-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889

TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 153:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Protein
SEQUENCE DESCRIPTION: SEQ ID NO: 153:
US-10-127-890-153

Query Match 23.9%: Score 26; DB 14; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.1e-17;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SALTOPASVSGSPGOSITISCTGTSS 27
DB 2 SALTOPASVSGSPGOSITISCTGTSS 27

RESULT 5

US-10-340-189-17
Sequence 17, Application US/10340189
Publication No. US20030229207A1
GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESSES:
ADDRESSEE: McAndrews, Heid & Malloy, Ltd.
STREET: 500 W. Madison Street, 34th Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/340,189
FILING DATE: 10-Jan-2003
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/245,202A
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/082,842
FILING DATE: 23-JUN-1993
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11023US07 / 200-71.P2.C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-340-189-17
Query Match 23.9%: Score 26; DB 15; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.1e-17;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SALTOPASVSGSPGOSITISCTGTSS 27
DB 2 SALTOPASVSGSPGOSITISCTGTSS 27

RESULT 6

US-10-325-696-17
Sequence 17, Application US/10325696
Publication No. US20040005630A1
GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESSES:
ADDRESSEE: McAndrews, Heid & Malloy, Ltd.
STREET: 500 West Madison Street, 34th Floor
CITY: Chicago
STATE: IL
COUNTRY: United States of America
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/325,696
FILING DATE: 18-Dec-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/097,980
FILING DATE: 16-JUN-1998
APPLICATION NUMBER: 08/107,669
FILING DATE: 13-AUG-1993
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Janet M. McNicholas, Ph.D.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11023US06/200-71.P1.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9050
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-325-696-17
Query Match 23.9%: Score 26; DB 15; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.1e-17;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SALTOPASVSGSPGOSITISCTGTSS 27
DB 2 SALTOPASVSGSPGOSITISCTGTSS 27

RESULT 7

US-10-026-925-98
Sequence 98, Application US/10026925
Publication No. US20030119056A1
GENERAL INFORMATION:
APPLICANT: LADNER, ROBERT C.
TITLE OF INVENTION: FOCUSED LIBRARIES OF GENETIC PACKAGES
FILE REFERENCE: DYAX/004

CURRENT APPLICATION NUMBER: US/10/026,925
CURRENT FILING DATE: 2002-05-28
NUMBER OF SEQ ID NOS: 99
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 98
LENGTH: 103
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: 2a2: H2 Human
OTHER INFORMATION: lambda-chain gene with stuffers in place of CDRs
US-10-026-925-98

Query Match 21.1%; Score 23; DB 14; Length 103;
Best Local Similarity 100.0%; Pred. No. 1,6e-14;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSALTQPASVSGSPGQSTITISC 23
DB 3 QSALTQPASVSGSPGQSTITISC 25

RESULT 8
US-09-563-222-94
Sequence 94, Application US/09563222
Publication No. US20030079253A1
GENERAL INFORMATION:
APPLICANT: Hact, Andrew
APPLICANT: Hein, Mich B.
TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
FILE REFERENCE: 310098,406
CURRENT APPLICATION NUMBER: US/09/563,222
CURRENT FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 197
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 94
LENGTH: 22
TYPE: PRT
ORGANISM: Homo sapien
US-09-563-222-94

Query Match 20.2%; Score 22; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 4,1e-14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSALTQPASVSGSPGQSTITISC 22
DB 1 QSALTQPASVSGSPGQSTITISC 22

RESULT 9
US-09-863-693-14
Sequence 14, Application US/09863693
Patent No. US20020062010A1
GENERAL INFORMATION:
APPLICANT: ARATHOON, R.
CARTER, P.J.
MERCHANT, A.M.
PRESTA, L.G.
TITLE OF INVENTION: METHOD FOR MAKING MULTISPECIFIC ANTIBODIES
HAVING HETEROMULTIMERIC AND COMMON COMPONENTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/863,693
FILING DATE: 23-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/070,166
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Conley, Delirdre L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: P1099R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-2066
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-863-693-14

Query Match 19.3%; Score 21; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 7,6e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 TASLTISGLQAEDEADYVCS 92
DB 12 TASLTISGLQAEDEADYVCS 32

RESULT 10
US-09-863-693-15
Sequence 15, Application US/09863693
Patent No. US20020062010A1
GENERAL INFORMATION:
APPLICANT: ARATHOON, R.
CARTER, P.J.
MERCHANT, A.M.
PRESTA, L.G.
TITLE OF INVENTION: METHOD FOR MAKING MULTISPECIFIC ANTIBODIES
HAVING HETEROMULTIMERIC AND COMMON COMPONENTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/863,693
FILING DATE: 23-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/070,166
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Conley, Delirdre L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: P1099R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-2066
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:

LENGTH: 50 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-863-693-15

Query Match 19.3%; Score 21; DB 9; Length 50;
Best Local Similarity 100.0%; Pred.No. 7.6e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 TASLTISGLQAEDEADYCCSS 92
DB 12 TASLTISGLQAEDEADYCCSS 32

RESULT 11
US-09-863-693-16
Sequence 16, Application US/09863693
Patent No. US20020062010A1
GENERAL INFORMATION:

APPLICANT: ARATHOON, R.
CARTER, P.J.
MERCHANT, A.M.
PRESTA, L.G.

TITLE OF INVENTION: METHOD FOR MAKING MULTISPECIFIC ANTIBODIES
HAVING HETEROMULTIMERIC AND COMMON COMPONENTS

NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:

ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco

STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/863,693
FILING DATE: 23-May-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/070,166
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Conley, Deirdre L.
REGISTRATION NUMBER: 36,487

REFERENCE/DOCKET NUMBER: P1099R1
TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-2066
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: Amino Acid

TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 16:

US-09-863-693-16

Query Match 19.3%; Score 21; DB 9; Length 50;
Best Local Similarity 100.0%; Pred.No. 7.6e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 TASLTISGLQAEDEADYCCSS 92
DB 12 TASLTISGLQAEDEADYCCSS 32

RESULT 12
US-09-863-693-17
Sequence 17, Application US/09863693

Patent No. US20020062010A1
GENERAL INFORMATION:

APPLICANT: ARATHOON, R.
CARTER, P.J.
MERCHANT, A.M.
PRESTA, L.G.

TITLE OF INVENTION: METHOD FOR MAKING MULTISPECIFIC ANTIBODIES
HAVING HETEROMULTIMERIC AND COMMON COMPONENTS

NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:

ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco

STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/863,693
FILING DATE: 23-May-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/070,166
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Conley, Deirdre L.
REGISTRATION NUMBER: 36,487

REFERENCE/DOCKET NUMBER: P1099R1
TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-2066
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: Amino Acid

TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 17:

US-09-863-693-17

Query Match 19.3%; Score 21; DB 9; Length 50;
Best Local Similarity 100.0%; Pred.No. 7.6e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 TASLTISGLQAEDEADYCCSS 92
DB 12 TASLTISGLQAEDEADYCCSS 32

RESULT 13
US-09-863-693-18

Sequence 18, Application US/09863693
Patent No. US20020062010A1
GENERAL INFORMATION:

APPLICANT: ARATHOON, R.
CARTER, P.J.
MERCHANT, A.M.
PRESTA, L.G.

TITLE OF INVENTION: METHOD FOR MAKING MULTISPECIFIC ANTIBODIES
HAVING HETEROMULTIMERIC AND COMMON COMPONENTS

NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:

ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco

STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/863,693
FILING DATE: 23-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/070,166
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Conley, Deirdre L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: P1099R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-2066
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-863-693-18

Query Match 19.3%; Score 21; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 7.6e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 TASLTISGLQAEDEADYYCSS 92
DB 12 TASLTISGLQAEDEADYYCSS 32

RESULT 14
US-09-863-693-19
Sequence 19 Application US/09863693
Patent No. US20020062010A1
GENERAL INFORMATION:
APPLICANT: ARATHOON, R.
CARTER, P.J.
MERCHANT, A.M.
PRESTA, L.G.
TITLE OF INVENTION: METHOD FOR MAKING MULTISPECIFIC ANTIBODIES
HAVING HETEROMULTIMERIC AND COMMON COMPONENTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/863,693
FILING DATE: 23-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/070,166
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Conley, Deirdre L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: P1099R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-2066
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-863-693-19

Query Match 19.3%; Score 21; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 7.6e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 TASLTISGLQAEDEADYYCSS 92
DB 12 TASLTISGLQAEDEADYYCSS 32

RESULT 15
US-09-863-693-20
Sequence 20 Application US/09863693
Patent No. US20020062010A1
GENERAL INFORMATION:
APPLICANT: ARATHOON, R.
CARTER, P.J.
MERCHANT, A.M.
PRESTA, L.G.
TITLE OF INVENTION: METHOD FOR MAKING MULTISPECIFIC ANTIBODIES
HAVING HETEROMULTIMERIC AND COMMON COMPONENTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/863,693
FILING DATE: 23-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/070,166
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Conley, Deirdre L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: P1099R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-2066
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-863-693-20

Query Match 19.3%; Score 21; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 7.6e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 TASLTISGLQAEDEADYYCSS 92
DB 12 TASLTISGLQAEDEADYYCSS 32

RESULT 16
US-09-863-693-21

Sequence 21, Application US/09863693
Patent No. US20020062010A1
GENERAL INFORMATION:
APPLICANT: ARATHOON, R.
CARTER, P.J.
MERCHANT, A.M.
PRESTA, L.G.
TITLE OF INVENTION: METHOD FOR MAKING MULTISPECIFIC ANTIBODIES
HAVING HETEROMULTIMERIC AND COMMON COMPONENTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/863,693
FILING DATE: 23-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/070,166
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Conley, Deirdre L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: P1099R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-2066
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-863-693-21
Query Match 19.3%; Score 21; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 7.6e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 72 TASLTISGLQAEADADYYCSS 92
Db 12 TASLTISGLQAEADADYYCSS 32
RESULT 17
US-09-863-693-22
Sequence 22, Application US/09863693
Patent No. US20020062010A1
GENERAL INFORMATION:
APPLICANT: ARATHOON, R.
CARTER, P.J.
MERCHANT, A.M.
PRESTA, L.G.
TITLE OF INVENTION: METHOD FOR MAKING MULTISPECIFIC ANTIBODIES
HAVING HETEROMULTIMERIC AND COMMON COMPONENTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/863,693
FILING DATE: 23-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/070,166
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Conley, Deirdre L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: P1099R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-2066
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-863-693-22
Query Match 19.3%; Score 21; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 7.6e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 72 TASLTISGLQAEADADYYCSS 92
Db 12 TASLTISGLQAEADADYYCSS 32
RESULT 18
US-09-373-403-14
Sequence 14, Application US/09373403
Publication No. US20030207346A1
GENERAL INFORMATION:
APPLICANT: ARATHOON, W. R.
CARTER, P.J.
MERCHANT, A.M.
PRESTA, L.G.
TITLE OF INVENTION: METHOD FOR MAKING MULTISPECIFIC ANTIBODIES HAVING
FILE REFERENCE: P1099C1 a
CURRENT APPLICATION NUMBER: US/09/373,403
CURRENT FILING DATE: 1999-08-12
PRIOR APPLICATION NUMBER: US 08/850,058
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 14
LENGTH: 50
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Recombinant
US-09-373-403-14
Query Match 19.3%; Score 21; DB 11; Length 50;
Best Local Similarity 100.0%; Pred. No. 7.6e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 72 TASLTISGLQAEADADYYCSS 92
Db 12 TASLTISGLQAEADADYYCSS 32
RESULT 19
US-09-373-403-15
Sequence 15, Application US/09373403
Publication No. US20030207346A1

RESULT 23
US-09-373-403-19
Sequence 19, Application US/09373403
Publication No. US20030207346A1
GENERAL INFORMATION:
APPLICANT: ARAHCOON, W. R.
APPLICANT: CARTER, P.U.
APPLICANT: MERCHANT, A.M.
APPLICANT: PRESTA, L.G.
TITLE OF INVENTION: METHOD FOR MAKING MULTISPECIFIC ANTIBODIES HAVING
TITLE OF INVENTION: HETEROMULTIMERIC AND COMMON COMPONENTS
FILE REFERENCE: P1099C1 a
CURRENT APPLICATION NUMBER: US/09/373,403
CURRENT FILING DATE: 1999-08-12

;; PRIOR APPLICATION NUMBER: US 08/850,058
;; PRIOR FILING DATE: 1997-05-02
;; NUMBER OF SEQ ID NOS: 26
;; SEQ ID NO 19
;; LENGTH: 50
;; TYPE: PRT
;; ORGANISM: Artificial sequence
;; FEATURE:
;; OTHER INFORMATION: Recombinant
US-09-373-403-19

Query Match 19.3%; Score 21; DB 11; Length 50;
Best Local Similarity 100.0%; Pred. No. 7.6e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 TASLTISGLQAEDEADYCCSS 92
Db 12 TASLTISGLQAEDEADYCCSS 32

RESULT 24

US-09-373-403-20
; Sequence 20, Application US/09373403
; Publication No. US20030207346A1
; GENERAL INFORMATION:
; APPLICANT: ARATHOON, W. R.
; APPLICANT: CARTER, P.J.
; APPLICANT: MERCHANT, A.M.
; APPLICANT: PRESTA, L.G.
; TITLE OF INVENTION: METHOD FOR MAKING MULTISPECIFIC ANTIBODIES HAVING
; FILE REFERENCE: P1099C1 a
; CURRENT APPLICATION NUMBER: US/09/373,403
; CURRENT FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: US 08/850,058
; PRIOR FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 20
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Recombinant
; NAME/KEY: Unsure
; LOCATION: 9
; OTHER INFORMATION: Unknown amino acid
US-09-373-403-20

Query Match 19.3%; Score 21; DB 11; Length 50;
Best Local Similarity 100.0%; Pred. No. 7.6e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 TASLTISGLQAEDEADYCCSS 92
Db 12 TASLTISGLQAEDEADYCCSS 32

RESULT 25

US-09-373-403-21
; Sequence 21, Application US/09373403
; Publication No. US20030207346A1
; GENERAL INFORMATION:
; APPLICANT: ARATHOON, W. R.
; APPLICANT: CARTER, P.J.
; APPLICANT: MERCHANT, A.M.
; APPLICANT: PRESTA, L.G.
; TITLE OF INVENTION: METHOD FOR MAKING MULTISPECIFIC ANTIBODIES HAVING
; FILE REFERENCE: P1099C1 a
; CURRENT APPLICATION NUMBER: US/09/373,403
; CURRENT FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: US 08/850,058
; PRIOR FILING DATE: 1997-05-02

;; NUMBER OF SEQ ID NOS: 26
;; SEQ ID NO 21
;; LENGTH: 50
;; TYPE: PRT
;; ORGANISM: Artificial sequence
;; FEATURE:
;; OTHER INFORMATION: Recombinant
US-09-373-403-21

Query Match 19.3%; Score 21; DB 11; Length 50;
Best Local Similarity 100.0%; Pred. No. 7.6e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 TASLTISGLQAEDEADYCCSS 92
Db 12 TASLTISGLQAEDEADYCCSS 32

Search completed: March 15, 2004, 07:45:17
Job time : 35 secs

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CM protein - protein search, using sw model

Run on: March 15, 2004, 07:39:39 ; Search time 38 Seconds
(without alignments)
905.039 Million cell updates/sec

Title: US-09-620-955b-4
Perfect score: 109
Sequence: 1 QSALTOPASVSGSQSGSITIT.....CSSFANSGLFGGKIVTVL 109

Scoring table: Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 199917

Minimum DB seq length: 0

Maximum DB seq length: 109

Post-processing: Listing first 100 summaries

Database :

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	10.1	17	4	Q9UC72 homo sapien
2	10	9.2	81	4	Q722E8
3	10	9.2	107	4	Q9UL81
4	10	9.2	107	4	Q96SA9
5	10	9.2	107	4	Q9NSD6
6	8	7.3	93	4	Q9UL76
7	8	7.3	101	4	Q81ZD8
8	8	7.3	107	4	Q9UL82
9	8	7.3	108	4	Q96SB0
10	7	6.4	109	4	Q9UL85
11	7	6.4	109	4	Q9UL78
12	6	5.5	24	5	Q9TWK4
13	6	5.5	53	5	Q967G7
14	6	5.5	57	10	Q7XIV6
15	6	5.5	57	16	Q9PNW1
16	6	5.5	60	10	Q7Y024

17	6	5.5	61	16	Q53965	Q53965 streptomyce
18	6	5.5	63	16	Q914Z8	Q914Z8 pseudomonas
19	6	5.5	63	16	Q7V7R8	Q7V7R8 prochloroco
20	6	5.5	68	16	Q7UWM3	Q7UWM3 rhodospirill
21	6	5.5	69	16	Q914H8	Q914H8 pseudomonas
22	6	5.5	69	16	Q8XBP2	Q8XBP2 escherichia
23	6	5.5	69	16	Q8BMP8	Q8BMP8 pseudomonas
24	6	5.5	71	16	Q89S16	Q89S16 bradyrhizob
25	6	5.5	71	16	Q82Z39	Q82Z39 enterococcu
26	6	5.5	72	5	Q9GEP2	Q9GEP2 ceenorthabdi
27	6	5.5	73	16	Q87Y28	Q87Y28 pseudomonas
28	6	5.5	76	16	Q83712	Q83712 enterococcu
29	6	5.5	80	2	Q7XIB4	Q7XIB4 leptospirill
30	6	5.5	87	12	Q69540	Q69540 human herpe
31	6	5.5	87	12	Q69538	Q69538 human herpe
32	6	5.5	90	4	Q14778	Q14778 homo sapien
33	6	5.5	91	16	Q88NJB	Q88NJB pseudomonas
34	6	5.5	95	2	Q7X105	Q7X105 xanthomonas
35	6	5.5	97	11	Q9UL76	Q9UL76 mus musculu
36	6	5.5	99	10	Q9W247	Q9W247 arabidopsi
37	6	5.5	99	11	Q9UL74	Q9UL74 mus musculu
38	6	5.5	100	6	Q77624	Q77624 bos taurus
39	6	5.5	101	11	Q9UL78	Q9UL78 mus musculu
40	6	5.5	103	11	Q9UL80	Q9UL80 mus musculu
41	6	5.5	103	12	Q81LH1	Q81LH1 white spot
42	6	5.5	103	16	Q92Z25	Q92Z25 rhizobium m
43	6	5.5	104	11	Q9UL82	Q9UL82 mus musculu
44	6	5.5	105	4	Q8WVU6	Q8WVU6 homo sapien
45	6	5.5	105	16	Q8XFX3	Q8XFX3 salmonella
46	6	5.5	107	11	Q9UL84	Q9UL84 mus musculu
47	6	5.5	107	15	Q7ZC22	Q7ZC22 human immun
48	6	5.5	107	15	Q7ZC22	Q7ZC22 mus musculu
49	6	5.5	108	11	Q8V1J0	Q8V1J0 mus musculu
50	6	5.5	109	6	Q9N0W5	Q9N0W5 cryciolagus
51	6	5.5	109	11	Q920B5	Q920B5 mus musculu
52	6	5.5	109	11	Q9ETI3	Q9ETI3 mus musculu
53	6	5.5	14	4	Q727E2	Q727E2 homo sapien
54	6	5.5	15	10	Q96924	Q96924 brassica ol
55	6	5.5	17	10	Q968E7	Q968E7 brassica ol
56	6	5.5	18	10	Q968L5	Q968L5 zea mays (m
57	6	5.5	19	10	Q96921	Q96921 brassica ol
58	6	5.5	20	5	Q26805	Q26805 trypanosoma
59	6	5.5	20	5	Q27385	Q27385 trypanosoma
60	6	5.5	20	6	Q9TR56	Q9TR56 sus scrofa
61	6	5.5	23	10	Q7Y0B6	Q7Y0B6 oryza sativ
62	6	5.5	24	5	Q8W734	Q8W734 leishmania
63	6	5.5	25	2	Q9UCQ0	Q9UCQ0 homo sapien
64	6	5.5	26	2	Q9RSK6	Q9RSK6 campylobact
65	6	5.5	26	12	Q9QRV0	Q9QRV0 hepatitis c
66	6	5.5	26	12	Q9QRV0	Q9QRV0 hepatitis c
67	6	5.5	28	2	Q05574	Q05574 prochloroch
68	6	5.5	29	2	Q938P6	Q938P6 borrelia bu
69	6	5.5	30	4	Q9H8G2	Q9H8G2 homo sapien
70	6	5.5	30	11	P97627	P97627 ractus norv
71	6	5.5	32	2	Q45534	Q45534 bacillus su
72	6	5.5	32	3	P78614	P78614 emericella
73	6	5.5	33	12	Q83672	Q83672 measles vir
74	6	5.5	34	16	Q8F7E7	Q8F7E7 leptospira
75	6	5.5	34	16	Q8F7E7	Q8F7E7 leptospira
76	6	5.5	35	13	Q45807	Q45807 clostridium
77	6	5.5	35	15	Q9PRP0	Q9PRP0 gallus gall
78	6	5.5	35	15	Q7SIE9	Q7SIE9 human immun
79	6	5.5	36	10	Q9ANQ4	Q9ANQ4 cryza sativ
80	6	5.5	37	16	Q8F7B5	Q8F7B5 leptospira
81	6	5.5	38	16	Q8KE41	Q8KE41 chlorobium
82	6	5.5	38	16	Q7UUM5	Q7UUM5 rhodospirill
83	6	5.5	39	16	Q8UEV3	Q8UEV3 agrobacteri
84	6	5.5	41	5	Q7X110	Q7X110 leptospirill
85	6	5.5	41	5	P91022	P91022 caenorhabdi
86	6	5.5	41	6	Q918B4	Q918B4 bos taurus
87	6	5.5	41	16	Q8FEK7	Q8FEK7 leptospira
88	6	5.5	41	16	Q8EJMT	Q8EJMT shewanella
89	6	5.5	41	16	Q87263	Q87263 pseudomonas
90	6	5.5	41	16	Q7VND1	Q7VND1 haemophilus

90 5 4.6 42 16 Q81MR8
 91 5 4.6 42 16 Q819L0
 92 5 4.6 43 16 Q8NV57
 93 5 4.6 44 3 Q8J1F0
 94 5 4.6 45 4 Q9UDH0
 95 5 4.6 45 4 Q8NEA2
 96 5 4.6 45 6 Q97730
 97 5 4.6 46 2 Q9EUR0
 98 5 4.6 46 2 Q9S604
 99 5 4.6 46 2 Q9F1F0
 100 5 4.6 46 2 Q7WXJ6

Q81MR8 bacillus an
 Q819L0 bacillus ce
 Q8NV57 scaphylococ
 Q8J1F0 fusarium sp
 Q9UDH0 homo sapien
 Q8NEA2 homo sapien
 Q97730 cabasacus u
 Q9EUR0 streptococc
 Q9S604 escherichia
 Q9F1F0 enterococcu
 Q7WXJ6 alcaligenes

ALIGNMENTS

RESULT 1
 Q9UC72 PRELIMINARY; PRT; 17 AA.
 AC Q9UC72;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Amyloid L (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95340562; PubMed=7615568;
 RA Castano E.M., Prelli F., Pras M., Frangione B.;
 RT "Apolipoprotein E carboxyl-terminal fragments are complexed to
 RT amyloids A and L. Implications for amyloidogenesis and Alzheimer's
 RT disease";
 RT J. Biol. Chem. 270:17610-17615 (1995).
 SQ SEQUENCE 17 AA; 1628 MW; E3FB99833638249 CRC64;

Query Match 10.1%; Score 11; DB 4; Length 17;
 Best Local Similarity 100.0%; Pred. No. 0.00032;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SALTOPASVS 12
 DB 1 SALTOPASVS 11

RESULT 2

Q7Z2E8 PRELIMINARY; PRT; 81 AA.
 AC Q7Z2E8;
 DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Rearranged V131 segment (Rearranged V131 gene segment)
 DE (Fragment).
 GN V13L.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Hodgkin lymphoma, and Mantle cell lymphoma;
 RA Tinsley M., Rosenquist R., Sundstrom C., Amin R.M., Kuppers R.,
 RA Hansmann M.L., Brautner A.;
 RT "Analysis of a clonally related mantle cell and Hodgkin lymphoma
 RT indicates Epstein-Barr virus infection of a Hodgkin/Reed-Sternberg
 RT cell precursor in a germinal center";
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ564423; CAD92030.1; -
 DR EMBL: AJ564424; CAD92030.1; -
 FT NON_TER 1

FT NON TER 81
 SQ SEQUENCE 81 AA; 8702 MW; CF71D466B794C9F CRC64;

Query Match 9.2%; Score 10; DB 4; Length 81;
 Best Local Similarity 100.0%; Pred. No. 0.015;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 QAEDEADLYC 90
 DB 59 QAEDEADLYC 68

RESULT 3

Q9UL81 PRELIMINARY; PRT; 107 AA.
 AC Q9UL81;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Myosin-reactive immunoglobulin light chain variable region
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus";
 RT Clin. Immunol. Immunopathol. 87:184-192 (1998).
 RL EMBL: AF035033; AAD56269.1; -
 DR HSP; P01607; IREI.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PSS0835; IG-LIKE; 1.
 FT NON_TER 1
 FT NON_TER 107
 SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 9.2%; Score 10; DB 4; Length 107;
 Best Local Similarity 100.0%; Pred. No. 0.019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 LTISGLQAE 84
 DB 73 LTISGLQAE 82

RESULT 4

Q96SA9 PRELIMINARY; PRT; 107 AA.
 AC Q96SA9;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
 DE variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98375893; PubMed=9712075;
 RA Adderson E.E., Shikman A.R., Ward K.B., Cunningham M.W.;
 RT "Molecular analysis of polyclonal monoclonal antibodies from
 RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
 RT antibody V region genes";

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RT J. Immunol. 161:2020-2031(1998).
DR EMBL; U95396; AAB68785.1; -.
DR PIR; B49047; B49047.
DR PIR; S34083; S34083.
DR PIR; S34086; S34086.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG-LIKE; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11520 MW; 4BB43B9C5B577F16 CRC64;

Query Match
Best Local Similarity 100.0%; Score 10; DB 4; Length 107;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 PGKAPKLLIY 51
DB 40 PGKAPKLLIY 49

RESULT 5
Q9NSD6 PRELIMINARY; PRT; 107 AA.
AC Q9NSD6;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphocytes;
RA Hohmann A.;
RT "Autoimmunity.";
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; I43092; AAA69746.2; -.
DR HSSP; P01709; 2MCG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG-LIKE; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11306 MW; A2B04B37187A5F00 CRC64;

Query Match
Best Local Similarity 100.0%; Score 10; DB 4; Length 107;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 QAEDADYYC 90
DB 76 QAEDADYYC 85

RESULT 6
Q9UL76 PRELIMINARY; PRT; 93 AA.
AC Q9UL76;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
DE "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035038; AAD56274.1; -.
DR HSSP; P01709; 2MCG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG-LIKE; 1.
FT NON_TER 1
FT NON_TER 93
SQ SEQUENCE 93 AA; 9596 MW; 2F3C1F6FPA6B90AF CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 4; Length 93;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 EDEADYYC 90
DB 67 EDEADYYC 74

RESULT 7
Q81ZD8 PRELIMINARY; PRT; 101 AA.
AC Q81ZD8;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Anti-thyroglobulin light chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Jang Y.-J., Chung J.-Y.;
RT "Isolation and Sequence Analysis of Monoclonal Anti-Hisone and Anti-
RT Thyroglobulin Single Chain Fv from SLE Patient by Phage Display.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY145444; AAN64328.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG-LIKE; 1.
FT NON_TER 1
FT NON_TER 101
SQ SEQUENCE 101 AA; 10374 MW; 1506C2D9AACBA793 CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 4; Length 101;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 NYVSWYQQ 40
DB 22 NYVSWYQQ 29

RESULT 8
Q9UL82 PRELIMINARY; PRT; 107 AA.
AC Q9UL82;
DT 01-MAY-2000 (TRENBLrel. 13, Created)

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DT 01-MAY-2000 (TReMBLrel. 13, last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, last annotation update)
 DE Myosin-reactive immunoglobulin light chain variable region
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9827139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus."
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035032; AAD56268.1; -.
 DR HSSP; P01703; 7PAB.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG-LIKE; 1.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 107 AA; 11445 MW; 52F0CC1AB26821DC CRC64;

Query Match 7.3%; Score 8; DB 4; Length 107;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 EDEADYYC 90
 |||||
 DB 80 EDEADYYC 87

RESULT 9
 Q96SBO PRELIMINARY; PRT; 108 AA.
 AC Q96SBO;
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, last annotation update)
 DE Anti-streptococcal/anti-myosin immunoglobulin lambda light chain
 DE variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9837593; PubMed=9712075;
 RA Adderson E.E., Shikman A.R., Ward K.E., Cunningham M.W.;
 RT "Molecular analysis of polyclonal monoclonal antibodies from
 rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
 antibody V region genes."
 RL U. Immunol. 161:2020-2031(1998).
 DR EMBL; U96394; AAB68783.1; -.
 DR PDB; 1KU4; 29-MAY-02.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG-LIKE; 1.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 108 AA; 11594 MW; F4B5DC478A043P48 CRC64;

Query Match 7.3%; Score 8; DB 4; Length 108;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 RFGSGSKG 70
 |||||

DB 62 RFGSGSKG 69

RESULT 10
 Q9UL85 PRELIMINARY; PRT; 109 AA.
 AC Q9UL85;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, last annotation update)
 DE Myosin-reactive immunoglobulin kappa chain variable region
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9827139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus."
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035029; AAD56265.1; -.
 DR PIR; D30609; D30609.
 DR HSSP; P80362; 1WTL.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG-LIKE; 1.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 109 AA; 11761 MW; FB1E43E7C7AFACCC CRC64;

Query Match 6.4%; Score 7; DB 4; Length 109;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 FGGGTXV 106
 |||||
 DB 99 FGGGTXV 105

RESULT 11
 Q9UL78 PRELIMINARY; PRT; 109 AA.
 AC Q9UL78;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, last annotation update)
 DE Myosin-reactive immunoglobulin light chain variable region
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9827139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus."
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035036; AAD56272.1; -.
 DR PIR; A30601; A30601.
 DR PIR; A30608; A30608.
 DR PIR; B30601; B30601.
 DR PIR; B30607; B30607.
 DR PIR; C30601; C30601.
 DR PIR; C30607; C30607.

DR PIR; C30608; C30608.
 DR PIR; D30601; D30601.
 DR PIR; D30607; D30607.
 DR PIR; D30608; D30608.
 DR PIR; F30607; F30607.
 DR PIR; F30608; F30608.
 DR PIR; G30601; G30601.
 DR PIR; G30608; G30608.
 DR PIR; H30607; H30607.
 DR PIR; H30608; H30608.
 DR PIR; I30601; I30601.
 DR PIR; PH0963; PH0963.
 DR PIR; PH0965; PH0965.
 DR PIR; S34096; S34096.
 DR HSSP; P80362; 1MTL.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON_TER 1
 FT SEQUENCE 109 AA; 11646 MW; 5F675C52ECTEE197 CRC64;

Query Match 6.4%; Score 7; DB 4; Length 109;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 FGGGTXV 106
 DB 99 FGGGTXV 105

RESULT 12
 Q9TWM4 PRELIMINARY; PRT; 24 AA.
 ID Q9TWM4;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Proximal collagen (Fragment).
 OS Mytilus edulis (Blue mussel).
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Periomorpha; Mytiloida;
 CC Mytilidae; Mytilidae; Mytilus.
 CX NCBI_TaxID=6550;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95230211; PubMed=7714453;
 RA Qin X., Waite J.H.,
 RT "Exotic collagen gradients in the byssus of the mussel Mytilus
 edulis.";
 RT J. Exp. Biol. 198;633-644(1995).
 DR InterPro; IPR008160; Collagen.
 SQ SEQUENCE 24 AA; 2054 MW; 29A3FB20799A705 CRC64;

Query Match 5.5%; Score 6; DB 5; Length 24;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 SGSPQ 16
 DB 9 SGSPQ 14

RESULT 13
 Q967G7 PRELIMINARY; PRT; 53 AA.
 ID Q967G7;
 AC 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Putative transporter protein (Fragment).
 GN ACRD.

OS Leishmania infantum.
 OC Eukaryota; Eukaryota; Kinetoplastida; Trypanosomatidae; Leishmania.
 CX NCBI_TaxID=5671;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LEM75;
 RA Reguera R.M., Balana-Fouce R., Perez-Perejo Y., Ordóñez-Sacudero D.;
 RT "Efflux pumps and drug resistance in Leishmania infantum."
 RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY033147; AAK53064.1;
 DR InterPro; IPR01036; Acrflvln_res.
 DR Pfam; PF00873; ACR_tran; 1.
 FT NON_TER 1
 FT SEQUENCE 53 AA; 5672 MW; 2A78BA166691BC5 CRC64;

Query Match 5.5%; Score 6; DB 5; Length 53;
 Best Local Similarity 100.0%; Pred. No. 18+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 SKSGDT 72
 DB 20 SKSGDT 25

RESULT 14
 Q7XIV6 PRELIMINARY; PRT; 57 AA.
 ID Q7XIV6;
 AC 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Hypothetical protein OJ1409_C08.23.
 GN OJ1409_C08.23
 OS Oryza sativa (Japonica cultivar-group). Embryophyta; Tracheophyta;
 OC Eukaryota; Viridiplantae; Streptophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 CX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nippondare;
 RA Sasaki T., Matsunoto T., Yamamoto K.;
 RT "Oryza sativa nippondare(GA3) genomic DNA, chromosome 7, BAC
 clone: OJ1409_C08.";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP003757; BAC79547.1;
 KM Hypothetical protein.
 SQ SEQUENCE 57 AA; 6041 MW; D3761B678PA5C1D4 CRC64;

Query Match 5.5%; Score 6; DB 10; Length 57;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 GDTASL 75
 DB 36 GDTASL 41

RESULT 15
 Q9PNM1 PRELIMINARY; PRT; 57 AA.
 ID Q9PNM1;
 AC 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Putative lipoprotein.
 GN C0978C.
 OS Campylobacter jejuni.
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
 OC Campylobacteraceae; Campylobacter.
 CX NCBI_TaxID=197;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=NCIC 11168;
 RX MEDLINE=20150912; PubMed=10688204;
 RA Parthill J., Wren B.W., Mungall K., Kestley J.M., Churcher C.,
 RA Basham D., Chillingworth T., Davies R.M., Felwell T., Holtroyd S.,
 RA Jagers K., Kariyasev A.V., Nucle S., Pallen M.J., Penn C.W.,
 RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
 RA Whitehead S., Barrett B.G.;
 RT "The genome sequence of the food-borne pathogen *Campylobacter jejuni*
 RT reveals hypervariable sequences.";
 RL Nature 403:665-668(2000).
 DR EMBL; AL139076; CAB73234.1; -;
 DR PIR; G81372; G81372.
 DR InterPro; IPR000437; Prok_110proct.S.
 DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
 KM Complete proteome.
 SQ SEQUENCE 57 AA; 6645 MW; 3C614BC78F7C5B9 CRC64;

Query Match 5.5%; Score 6; DB 16; Length 57;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 GINSNF 64
 DB 23 GINSNF 28

RESULT 16
 ID Q7Y024 PRELIMINARY; PRT; 60 AA.
 AC Q7Y024;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein OJ1112_G08.18.
 GN OJ1112_G08.18.
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Eriophytidae; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriophytidae; Oryzae; Oryza.
 OX NCBI_Taxid=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Buehl C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
 RA Overton II L.L., Tsilirtz T., Kim M.M., Bera J.U., Jin S.S.,
 RA Padroch D.W., Tallon L.J., Koo H., Ziemann V., Hsiao J., Blunt S.,
 RA Vanaken S.S., Riedmuller S.B., Uteback T.T., Feldey T.V.,
 RA Yang Q.Q., Haas B.U., Sun B.B., Peterson J.J., Quackenbush J.,
 RA White O., Salzberg S.L., Fraser C.M.;
 RA "Oryza sativa chromosome 3 BAC OJ1112_G08 genomic sequence.";
 RT Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 RL [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Buehl R.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC135225; AAP68359.1; -;
 KM Hypothetical protein.
 SQ SEQUENCE 60 AA; 6591 MW; 48C4E1775DE8F4FA CRC64;

Query Match 5.5%; Score 6; DB 10; Length 60;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 91 SSFANS 96
 DB 33 SSFANS 38

RESULT 17
 ID Q53965 PRELIMINARY; PRT; 61 AA.
 AC Q53965

AC Q53965;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE EXCISIONASE.
 XS OR SC04616 OR SC039.16C.
 OS Streptomyces coelicolor.
 OG Plasmid pR11724.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycetaceae; Streptomyces.
 OX NCBI_Taxid=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC PLASMID-PRI1724;
 RX MEDLINE=9325953; PubMed=8387993;
 RA Braach M.A., Pettis G.S., Lee S.C., Cohen S.N.;
 RT "Localization and nucleotide sequences of genes mediating site-
 RT specific recombination of the SLP1 element in *Streptomyces lividans*."
 RT J. Bacteriol. 175:3067-3074(1993).
 RL [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RP Brown S.P., Harris D.;
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Cerdano A.M., Parkhill J., Barrett B.G., Rajandream M.A.;
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RX MEDLINE=97000351; PubMed=8843436;
 RA Redenbach M., Kleser H.M., Denapate D., Eichner A., Cullum J.,
 RA Knaehtl H., Hopwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 RT the 8 Mb *Streptomyces coelicolor* A3(2) chromosome.";
 RL Mol. Microbiol. 21:77-96(1996).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RX MEDLINE=21996410; PubMed=12000953;
 RA Bentley S.D., Chater K.F., Cerdano A.M., Parkhill J., Kleser H.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.H., Kleser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietorrek A., Woodward J., Barrett B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete *Streptomyces*
 RT *coelicolor* A3(2).";
 RL Nature 417:141-147(2002).
 DR EMBL; X71358; CAA50493.1; -;
 DR EMBL; AL939120; CAC08269.1; -;
 DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
 KM Plasmid; Complete proteome.
 SQ SEQUENCE 61 AA; 7103 MW; CCC67B2FDD173512 CRC64;

Query Match 5.5%; Score 6; DB 16; Length 61;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 GXAPRL 48
 DB 30 GXAPRL 35

RESULT 18
 ID Q91428 PRELIMINARY; PRT; 63 AA.
 AC Q91428

DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Probable cold-shock protein.
 GN PA0961.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE=2043737; PubMed=10984043;
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Lathig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Sater M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
 RT opportunistic pathogen.";
 RT Nature 406:959-964(2000).
 RL Nature 406:959-964(2000).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE COLD-SHOCK DOMAIN (CSD) FAMILY.
 DR EMBL; AE004530; AAC04350.1; -.
 DR PIR; C83524; C83524.
 DR HSSP; P41016; 1C90.
 DR GO; GO:0003677; P:DNA binding; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR002059; Cold_shock.
 DR InterPro; IPR008994; Nucleic_acid_OB.
 DR Pfam; PF00313; CSD; 1.
 DR PRINTS; PR00050; COLDSHOCK.
 DR ProDom; PD000621; Cold_shock; 1.
 DR SMART; SM00357; CSP; 1.
 DR PROSITE; PS00352; COLD_SHOCK; 1.
 DR Activator; DNA-binding; Transcription regulation; Complete proteome.
 KW SEQUENCE 63 AA; 7281 MW; 1219B2AB9C6B6808 CRC64;
 SQ
 Query Match 5.5%; Score 6; DB 16; Length 63;
 Best Local Similarity 100.0%; Pred.No.2.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 79 GLOAED 84
 DB 52 GLOAED 57
 RESULT 19
 ID Q7V7R8 PRELIMINARY; PRT; 63 AA.
 AC Q7V7R8;
 DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN PMT0670.
 OS Prochlorococcus marinus (strain MIT 9313).
 OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcales;
 OC Prochlorococcus.
 OX NCBI_TaxID=74547;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE=22825698; PubMed=12917642;
 RA Roop G., Larimer F.W., Lamerdin J., Malfatti S., Chain P.,
 RA Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
 RA Johnson Z.I., Land W., Lindell D., Post A.F., Regala W., Shah M.,
 RA Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
 RA Webb E.A., Zinser E.R., Chisholm S.W.;
 RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic
 RT niche differentiation.";
 RT Nature 424:1042-1047(2003).
 RL Nature 424:1042-1047(2003).
 DR EMBL; BX572097; CAE20845.1; -.

KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 63 AA; 7090 MW; E8DC5102ECC593B CRC64;
 Query Match 5.5%; Score 6; DB 16; Length 63;
 Best Local Similarity 100.0%; Pred.No.2.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 65 SGRKSG 70
 DB 26 SGRKSG 31
 RESULT 20
 ID Q7UWM3 PRELIMINARY; PRT; 68 AA.
 AC Q7UWM3;
 DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN RB1931.
 OS Rhodospirillum rubrum.
 OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
 OC Planctomycetaceae; Firelulula.
 OX NCBI_TaxID=117;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1;
 RX MEDLINE=22735913; PubMed=12835416;
 RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
 RA Ludwig W., Gade D., Beck A., Borzym K., Heilmann K., Rabus R.,
 RA Schleutner H., Amann R., Reinhardt R.;
 RT "Complete genome sequence of the marine planctomycete Firelulula sp.
 RT strain 1.";
 RT Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
 DR EMBL; BX294136; CAD72339.1; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 68 AA; 7494 MW; 7EC1DF98B5F67C CRC64;
 Query Match 5.5%; Score 6; DB 16; Length 68;
 Best Local Similarity 100.0%; Pred.No.2.3e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 74 SLTISG 79
 DB 3 SLTISG 8
 RESULT 21
 ID Q914H8 PRELIMINARY; PRT; 69 AA.
 AC Q914H8;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Probable cold-shock protein.
 GN PA1159.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE=2043737; PubMed=10984043;
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Lathig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Sater M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
 RT opportunistic pathogen.";

RL Nature 406:959-964(2000).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE COLD-SHOCK DOMAIN (CSD) FAMILY.
 DR EMBL; AE004546; AAG04548.1; -.
 DR PIR; D83500; D83500.
 DR HSSP; P41016; 1C90.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR002059; Cold_shock.
 DR InterPro; IPR008994; Nucleic_acid_OB.
 DR Pfam; PF00313; CSD; 1.
 DR PRINTS; PR00050; COLDSHOCK.
 DR ProDom; PD000621; Cold_shock; 1.
 DR SMART; SM00357; CSP_1_shock; 1.
 DR PROSITE; PS00352; COLD_SHOCK; 1.
 DR Activator; DNA-binding; Transcription regulation; Complete proteome.
 SQ SEQUENCE 69 AA; 7725 MW; 00D7304061D64D2 CRC64;

Query Match 5.5%; Score 6; DB 16; Length 69;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 GLOAED 84
 DB 60 GLOAED 65

RESULT 22
 ID Q88MP2 PRELIMINARY; PRT; 69 AA.
 AC Q88MP2;
 DT 01-MAR-2002 (TRENBLrel. 20, Created)
 DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Y8B protein.
 GN Y8B OR Z0783 OR ECG0675.
 OS Escherichia coli O157:H7.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 CX NCBI_TaxID=83334;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O157:H7 / EDU933 / ATCC 700927;
 RX MEDLINE=21074935; PubMed=11206551;
 RA Pena N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
 RA Postel G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
 RA Grobeck E.J., Davis N.W., Lim A., Dimalanta B.T., Potamous K.,
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
 RA Welch R.A., Blattner F.R.;
 RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";
 RL Nature 409:529-533(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O157:H7 / RIMD 0509952;
 RX MEDLINE=21156231; PubMed=11258796;
 RA Hayashi T., Makino K., Oniishi M., Kurokawa K., Ishii K., Yokoyama K.,
 RA Han C.-G., Ono S., Nakayama K., Murata T., Tanaka M., Tobe T.,
 RA Iida T., Takami H., Honda T., Sasaki G., Ogasawara N., Yasunaga T.,
 RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
 RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
 RT O157:H7 and genomic comparison with a laboratory strain K-12.";
 RL DNA Res. 8:11-22(2001).
 DR EMBL; AE005242; AAG54571.1; -;
 DR EMBL; AP002552; BAB34098.1; -;
 DR PIR; A24995; QCECP7.
 DR PIR; C90713; C90713.
 DR PIR; G85563; G85563.
 DR InterPro; IPR004394; Icjap.
 DR Pfam; PF02410; DUF143; 1.
 DR TIGRfams; TIGR00090; TIGR00090; 1.
 KW Complete proteome.
 SQ SEQUENCE 69 AA; 7678 MW; A470FC77D9207E12 CRC64;

Query Match 5.5%; Score 6; DB 16; Length 69;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CTGTSS 27
 DB 4 CTGTSS 9

RESULT 23
 ID Q88MP8 PRELIMINARY; PRT; 69 AA.
 AC Q88MP8;
 DT 01-JUN-2003 (TRENBLrel. 24, Created)
 DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Cold shock protein CspA.
 GN CSPA-1 OR P1522.
 OS Pseudomonas putida (strain KT2440).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 CX NCBI_TaxID=160486;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22423060; PubMed=12534463;
 RA Nelson K.E., Weiner C., Paulsen I.T., Dodson R.J., Hilbert H.,
 RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
 RA Brinkac L., Bennett M., DeBoy R.T., Daugherty S., Kolonay J.,
 RA Madupu R., Nelson W., White O., Peterson J., Kouri H., Hance I.,
 RA Chris Lee P., Holtzapple E., Scanlan D., Tyrn K., Moazzes A.,
 RA Uterback T., Rizzo M., Lee K., Kosack D., Moesli D., Medler H.,
 RA Lauber J., Stjepandic D., Hoheisel J., Straetz M., Helm S.,
 RA Klewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tsemmler B.,
 RA Fraser C.M.;
 RT "Complete genome sequence and comparative analysis of the
 RT metabolically versatile Pseudomonas putida KT2440.";
 RL Environ. Microbiol. 4:799-808(2002).
 DR EMBL; AB016779; AAN67143.1; -;
 DR TIGR; P15522; -;
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR002059; Cold_shock.
 DR InterPro; IPR008994; Nucleic_acid_OB.
 DR Pfam; PF00313; CSD; 1.
 DR PRINTS; PR00050; COLDSHOCK.
 DR PROSITE; PS00352; COLD_SHOCK; 1.
 KW Complete proteome.
 SQ SEQUENCE 69 AA; 7673 MW; 5A7E14A10FDA954A CRC64;

Query Match 5.5%; Score 6; DB 16; Length 69;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 GLOAED 84
 DB 60 GLOAED 65

RESULT 24
 ID Q89S16 PRELIMINARY; PRT; 71 AA.
 AC Q89S16;
 DT 01-JUN-2003 (TRENBLrel. 24, Created)
 DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Bsr2414 protein.
 GN BSR2414.
 OS Bradyrhizobium japonicum.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae; Bradyrhizobium.
 CX NCBI_TaxID=375;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=USDA 110;
 RX MEDLINE=22484998; PubMed=12597275;
 RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiyama T.,
 RA Sasamoto S., Watanabe A., Ideawa K., Iritaguchi M., Kawashima K.,
 RA Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
 RA Tabata S.;
 RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
 RT Bradyrhizobium japonicum USDA110.";
 RL DNA Res. 9:189-187(2002).
 DR EMBL; AP005943; BAC4/679.1; -;
 DR GO; GO:0000155; F:two-component sensor molecule activity; IEA.
 DR GO; GO:0000160; P:two-component signal transduction system (p. . .; IEA.
 DR InterPro; IPR000700; PAS-asso_C.
 DR PROSITE; PS50113; PAC; 1.
 KM Complete proteome.
 SQ SEQUENCE 71 AA; 7501 MW; CC91E64E2B507DC5 CRC64;

Query Match 5.5%; Score 6; DB 16; Length 71;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 73 ASLTTIS 78
 |||||
 Db 61 ASLTTIS 66

RESULT 25

082Z39 PRELIMINARY; PRT; 71 AA.
 AC 082Z39;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein.
 GN EF3239.
 OS Enterococcus faecalis (Streptococcus faecalis).
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 OX NCBI_TaxID=1351;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=V583 / ATCC 700802;
 RX MEDLINE=2250857; PubMed=1263927;
 RA Paulsen I.T., Banerjee I., Myers G.S.A., Nelson K.E., Seshadri R.,
 RA Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
 RA Tettelin H., Dodson R.J., Umayam L., Brinkac L., Beanan M.,
 RA Daugherty S., DeBoy R.T., Durkin S., Kolonay J., Madupu R., Nelson W.,
 RA Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,
 RA Utecherback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.;
 RT "Role of mobile DNA in the evolution of vancomycin-resistant
 RT Enterococcus faecalis.";
 RL Science 299:2071-2074(2003).
 DR EMBL; AB016957; AAO82907.1; -;
 DR TIGR; EF3239; -;
 KM Hypothetical protein; Complete proteome.
 SQ SEQUENCE 71 AA; 7931 MW; 5719F0029D89F7AB CRC64;

Query Match 5.5%; Score 6; DB 16; Length 71;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 19 ITISCT 23
 |||||
 Db 40 ITISCT 45

Search completed: March 15, 2004, 07:43:27
 Job time : 43 secs

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OM protein - protein search, using sw model

Run on: March 15, 2004, 07:39:09 ; Search time 17 Seconds
(without alignments)
333.862 Million cell updates/sec

Title: US-09-620-955b-4
Perfect score: 109
Sequence: 1 OSALTOPASVSGSPGOSITL.....CSSFANSGLPGGKRVTVL 109

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 17605

Minimum DB seq length: 0

Maximum DB seq length: 109

Post-processing: Listing first 100 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	17.4	109	1	LV2E_HUMAN
2	12	11.0	103	1	LV1E_HUMAN
3	11	10.1	108	1	KV1B_HUMAN
4	11	10.1	108	1	KV1P_HUMAN
5	10	9.2	107	1	LV4C_HUMAN
6	10	9.2	108	1	KV1K_HUMAN
7	10	9.2	108	1	KV1O_HUMAN
8	10	9.2	108	1	KV5R_MOUSE
9	10	9.2	108	1	KV5S_MOUSE
10	10	9.2	108	1	KV5T_MOUSE
11	10	9.2	108	1	LV3A_HUMAN
12	10	9.2	108	1	KV1T_HUMAN
13	9	8.3	109	1	KV1F_HUMAN
14	8	7.3	108	1	KV1L_HUMAN
15	8	7.3	109	1	LV1I_HUMAN
16	8	7.3	109	1	LV1I_HUMAN
17	8	7.3	109	1	LV1I_HUMAN
18	8	7.3	109	1	LV1I_HUMAN
19	8	7.3	109	1	LV1I_HUMAN
20	8	7.3	109	1	LV1I_HUMAN
21	8	7.3	109	1	LV1I_HUMAN
22	8	7.3	109	1	LV1I_HUMAN
23	8	7.3	109	1	LV1I_HUMAN
24	8	7.3	109	1	LV1I_HUMAN
25	8	7.3	109	1	LV1I_HUMAN
26	8	7.3	109	1	LV1I_HUMAN
27	8	7.3	109	1	LV1I_HUMAN
28	8	7.3	109	1	LV1I_HUMAN
29	8	7.3	109	1	LV1I_HUMAN
30	8	7.3	109	1	LV1I_HUMAN
31	8	7.3	109	1	LV1I_HUMAN
32	8	7.3	109	1	LV1I_HUMAN
33	8	7.3	109	1	LV1I_HUMAN

34	107	1	KV6D_MOUSE	P01678	mus musculus
35	108	1	KV0S_RABIT	P01686	oryctolagus
36	108	1	KV06_RABIT	P01687	oryctolagus
37	108	1	KV07_RABIT	P01688	oryctolagus
38	108	1	KV08_RABIT	P01689	oryctolagus
39	108	1	KV1A_HUMAN	P01593	homo sapien
40	108	1	KV1C_HUMAN	P01595	homo sapien
41	108	1	KV1E_HUMAN	P01597	homo sapien
42	108	1	KV1G_HUMAN	P01599	homo sapien
43	108	1	KV1H_HUMAN	P04430	homo sapien
44	108	1	KV1J_HUMAN	P01643	mus musculus
45	108	1	KV5J_MOUSE	P01644	mus musculus
46	108	1	KV5K_MOUSE	P01645	mus musculus
47	108	1	KV5L_MOUSE	P01646	mus musculus
48	108	1	KV5M_MOUSE	P01647	mus musculus
49	108	1	KV5N_MOUSE	P01648	mus musculus
50	108	1	KV5P_MOUSE	P01649	mus musculus
51	108	1	KV5U_MOUSE	P04946	mus musculus
52	109	1	KV14_RABIT	P01695	oryctolagus
53	109	1	KV1D_HUMAN	P01593	homo sapien
54	12	1	HCY1_CARPA	P03176	carcinus ma
55	27	1	LIPS_BOVIN	P16386	bos taurus
56	35	1	SCKB_PANIN	P55928	pandinus im
57	47	1	FLGD_YEREN	P55927	pandinus im
58	47	1	SCKA_PANIN	P01525	homo sapien
59	51	1	INEL_HUMAN	P42625	escherichia
60	54	1	YHAL_ECOLI	P44492	baecillus su
61	57	1	YOCO_BACSU	P03316	treponema p
62	58	1	Y293_TREPA	P04492	treponema p
63	59	1	SSH1_BACRA	P01687	baecillus an
64	59	1	SSH1_BACRA	P01687	baecillus an
65	62	1	SSH1_BACRA	P01687	baecillus an
66	63	1	CE3E_HYPCU	P07071	hyphantaia
67	64	1	PIPF_BOVIN	P04004	bos taurus
68	66	1	R24E_HALMA	P14116	halorcula
69	75	1	RL3I_CHUTE	P02036	cavia porce
70	77	1	PACT_CAVPO	P02036	cavia porce
71	77	1	SEGC_CORGL	P02036	corynebacte
72	77	1	SEGC_MYCLE	P02036	mycobacteri
73	77	1	SEGC_MYCTU	P02036	mycobacteri
74	78	1	DSVD_DRSYH	P02036	desulfobidr
75	78	1	RPOH_METAC	P02036	methanosarc
76	78	1	RPOH_METVA	P02036	methanosarc
77	78	1	RPOH_METVA	P02036	methanosarc
78	78	1	RPOH_METVA	P02036	methanosarc
79	80	1	CD24_HUMAN	P02036	homo sapien
80	80	1	CD24_HUMAN	P02036	homo sapien
81	80	1	CD24_HUMAN	P02036	homo sapien
82	80	1	CD24_HUMAN	P02036	homo sapien
83	80	1	CD24_HUMAN	P02036	homo sapien
84	80	1	CD24_HUMAN	P02036	homo sapien
85	80	1	CD24_HUMAN	P02036	homo sapien
86	80	1	CD24_HUMAN	P02036	homo sapien
87	80	1	CD24_HUMAN	P02036	homo sapien
88	80	1	CD24_HUMAN	P02036	homo sapien
89	80	1	CD24_HUMAN	P02036	homo sapien
90	80	1	CD24_HUMAN	P02036	homo sapien
91	80	1	CD24_HUMAN	P02036	homo sapien
92	80	1	CD24_HUMAN	P02036	homo sapien
93	80	1	CD24_HUMAN	P02036	homo sapien
94	80	1	CD24_HUMAN	P02036	homo sapien
95	80	1	CD24_HUMAN	P02036	homo sapien
96	80	1	CD24_HUMAN	P02036	homo sapien
97	80	1	CD24_HUMAN	P02036	homo sapien
98	80	1	CD24_HUMAN	P02036	homo sapien
99	80	1	CD24_HUMAN	P02036	homo sapien
100	80	1	CD24_HUMAN	P02036	homo sapien

ALIGNMENTS

RESULT 1

LV2E_HUMAN
ID LV2E_HUMAN STANDARD; PRT; 109 AA.
AC P01708;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig lambda chain V-II region BUR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=8006606; PubMed=113407;
RA Infante A.J., Putnam F.W.;
RT "Primary structure of a human IgA lambda light chain (Bur).";
RL J. Biol. Chem. 254:9006-9016(1979).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE KERN+ AND MCG+ MARKERS.
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A01974; L2HUBR.
DR HSSP; P01709; 2MCG.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG_1.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; Pyroliadone carboxylic acid.
KW DOMAIN 1 106
FT MOD_RES 1 1
FT DISULFID 22 90
FT SITE 91 91
FT SITE APPEARS TO BE A FREE BUT UNREACTIVE
FT SITE SULFHYDRYL GROUP.
FT NON_TER 109 109
FT SEQUENCE 109 AA; 11506 MW; BPD8AE1C5D267FAB CRC64;
SQ
Query Match 17.4%; Score 19; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 6.6e-13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 72 TASLTISGLQAEDEADYYC 90
DB 72 TASLTISGLQAEDEADYYC 90

RESULT 2
LV2E_HUMAN
ID LV2E_HUMAN STANDARD; PRT; 103 AA.
AC P01703;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig lambda chain V-I region NEMM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=74109253; PubMed=4814727;
RA Chen B.V., Poljak R.J.;
RT "Amino acid sequence of the (lambda) light chain of a human myeloma immunoglobulin (IgG New).";
RL Biochemistry 13:1295-1302(1974).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=78066916; PubMed=618887;
RA Saul F.A., Amzel L.M., Poljak R.J.;

RT "Preliminary refinement and structural analysis of the Fab fragment from human immunoglobulin new at 2.0-A resolution.";
RL J. Biol. Chem. 253:585-597(1978).
CC -1- MISCELLANEOUS: THE STRUCTURE OF THE FAB FRAGMENT OF THE IGG1 MYELOMA PROTEIN NEMM WAS DETERMINED.
CC -1- MISCELLANEOUS: THE ABSENCE OF SEVEN RESIDUES FOUND IN OTHER LAMBDA CHAINS WAS CONFIRMED BY X-RAY CRYSTALLOGRAPHIC ANALYSIS.
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE OZ+ MARKER.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A01968; L1HUNM.
DR PDB; 7FAB; 31-JAN-94.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; 3D-structure; Pyroliadone carboxylic acid.
KW DOMAIN 1 99
FT MOD_RES 1 1
FT STRAND 4 5
FT STRAND 9 12
FT STRAND 14 15
FT STRAND 18 23
FT STRAND 26 28
FT STRAND 29 31
FT HELIX 32 32
FT TURN 36 40
FT STRAND 42 43
FT TURN 47 48
FT STRAND 52 53
FT TURN 57 62
FT STRAND 63 64
FT TURN 65 70
FT STRAND 75 77
FT HELIX 79 87
FT STRAND 88 89
FT TURN 90 94
FT STRAND 97 101
FT NON_TER 103 103
FT SEQUENCE 103 AA; 10904 MW; 32727AD731AE7584 CRC64;
SQ
Query Match 11.0%; Score 12; DB 1; Length 103;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 79 GLQAEDEADYYC 90
DB 72 GLQAEDEADYYC 83

RESULT 3
KV2B_HUMAN
ID KV2B_HUMAN STANDARD; PRT; 108 AA.
AC P01554;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig kappa chain V-I region AV.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=72189444; PubMed=5028201;
RA Schenck H., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones protein Au).";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).

RN [2]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE=77022433; PubMed=1234024;
 RA Fellhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
 RA Schwaiger P., Steigemann W., Schramm H.J.;
 RT "The structure determination of the variable portion of the
 RT Bence-Jones protein Au."
 RL Biophys. Struct. Mech. 1:139-146(1975).
 CC -1- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY
 CC MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V
 CC REGION OF THE KAPPA CHAIN REI.
 CC -1- MISCELLANEOUS: THIS IS A Bence-Jones protein.
 CC PIR: A91653; KIHUAV.
 DR PDB: 1JVS; 30-JAN-02.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003596; IG_v.
 DR Pfam: PF00047; IG_1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 107 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11939 MW; E801187EE6F6B9 CRC64;

 Query Match 10.1%; Score 11; DB 1; Length 108;
 Best Local Similarity 100.0%; Pred. No. 0.00022; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 42 PGKAPKLLIYD 52
 DB 40 PGKAPKLLIYD 50

 RESULT 4
 KVIP_HUMAN STANDARD; PRT; 108 AA.
 ID KVIP_HUMAN
 AC P01608;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region Roy.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=68362076; PubMed=5595110;
 RA Hilschmann N.;
 RT "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and
 RT Cum.)";
 RL Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
 CC [2]
 RP REVISIONS TO 39 AND 41.
 RA Hilschmann N., Barnikol H.V., Hess M., Langer B., Ponstingl H.,
 RA Steinmetz-Kayne M., Suter L., Watanabe S.;
 RL (in) Franek F., Shugar D. (eds.);
 RL Gamma globulins: structure and function, pp.57-74, Academic Press,
 RL New York (1969).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
 CC MARKER.
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.

DR PIR: A91638; KIHURY.
 DR HSP: P80362; 1WTL.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003596; IG_v.
 DR Pfam: PF00047; IG_1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 107 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11782 MW; F5ACEDE5A313DF3A CRC64;

 Query Match 10.1%; Score 11; DB 1; Length 108;
 Best Local Similarity 100.0%; Pred. No. 0.00022; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 42 PGKAPKLLIYD 52
 DB 40 PGKAPKLLIYD 50

 RESULT 5
 LV4C_HUMAN STANDARD; PRT; 107 AA.
 ID LV4C_HUMAN
 AC P01717;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig lambda chain V-IV region H1.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=78187276; PubMed=418804;
 RA Lopez de Castro J.A., Chiu Y.-Y.H., Poljak R.J.;
 RT "Amino acid sequence of the variable region of the light (lambda)
 RT chain from human myeloma cryoglobulin IgG H1.";
 RL Biochemistry 17:1718-1723(1978).
 CC -1- MISCELLANEOUS: THE SEQUENCE OF THE C REGION IS APPARENTLY
 CC IDENTICAL WITH THAT OF HUMAN SH LAMBDA CHAIN EXCEPT IN HAVING
 CC 155-ILE (H1 NUMBERING) INSTEAD OF VAL.
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC PIR: A01983; L4VHUL.
 DR HSP: P80748; 2UOI.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003596; IG_v.
 DR Pfam: PF00047; IGV; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 97 IG-LIKE.
 FT NON TER 107 107
 SQ SEQUENCE 107 AA; 11517 MW; A5C8A8FE0C0C590A CRC64;

 Query Match 9.2%; Score 10; DB 1; Length 107;
 Best Local Similarity 100.0%; Pred. No. 0.0025; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 QAEDEADYYC 90
 |||||
 DB 78 QAEDEADYYC 87

RESULT 6
 KVIK HUMAN STANDARD; PRT; 108 AA.
 AC P01603; 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region Ka.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NCB1_TaxID=9606;
 RN (1)
 RP SEQUENCE.
 RX MEDLINE=76189965; PubMed=818073;
 RA Shukoda T.;
 RT "Comparative structural studies on the light chains of human immunoglobulins. I. Protein Ka with the inv(3) alleotypic marker."
 RL J. Biochem. 77:1277-1296(1975).
 CC -1- MISCELLANEOUS; THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS; This is a Bence-Jones protein.
 DR PIR; A01869; KIHUKA.
 DR HSSP; P80362; 1WTL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; P:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG_V.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IG_1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 2 34 FRAMEWORK-2.
 FT DOMAIN 3 49 FRAMEWORK-3.
 FT DOMAIN 4 56 FRAMEWORK-4.
 FT DOMAIN 5 77 FRAMEWORK-5.
 FT DOMAIN 6 88 FRAMEWORK-6.
 FT DOMAIN 7 97 FRAMEWORK-7.
 FT DOMAIN 8 107 FRAMEWORK-8.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11900 MW; 768839FBD5A2F4B CRC64;
 Query Match 9.2%; Score 10; DB 1; Length 108;
 Best Local Similarity 100.0%; Pred. No. 0.0025;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RA Palm W.; Hilschmann N.;
 RT "The primary structure of a crystalline monoclonal immunoglobulin kappa-type L-chain, subgroup I (Bence-Jones protein Rel); isolation and characterization of the tryptic peptides; the complete amino acid sequence of the protein; a contribution to the elucidation of the three-dimensional structure of antibodies, in particular their combining site";
 RT Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
 RL (2)
 RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RP MEDLINE=76039968; PubMed=1182131;
 RA Epp O.; Latman E.B.; Schiffer M.; Huber R.; Palm W.;
 RT "The molecular structure of a dimer composed of the variable portions of the Bence-Jones protein Rel refined at 2.0-A resolution."
 RL Biochemistry 14:4945-4952(1975).
 CC -1- MISCELLANEOUS; THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.
 CC -1- MISCELLANEOUS; This is a Bence-Jones protein.
 DR PIR; A91663; KIHURE.
 DR PDB; 1RE1; 17-FEB-84.
 DR PDB; 1AR2; 12-NOV-97.
 DR PDB; 1BMW; 29-DEC-99.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; P:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG_V.
 DR InterPro; IPR003596; IG_1.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IG_1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 2 34 FRAMEWORK-2.
 FT DOMAIN 3 49 FRAMEWORK-3.
 FT DOMAIN 4 56 FRAMEWORK-4.
 FT DOMAIN 5 77 FRAMEWORK-5.
 FT DOMAIN 6 88 FRAMEWORK-6.
 FT DOMAIN 7 97 FRAMEWORK-7.
 FT DOMAIN 8 107 FRAMEWORK-8.
 FT DISULFID 23 88
 FT STRAND 4 7
 FT STRAND 10 13
 FT STRAND 15 16
 FT STRAND 19 25
 FT STRAND 30 31
 FT STRAND 33 38
 FT STRAND 40 41
 FT STRAND 44 49
 FT STRAND 50 52
 FT STRAND 53 54
 FT STRAND 56 57
 FT STRAND 60 61
 FT STRAND 62 67
 FT STRAND 68 69
 FT STRAND 70 75
 FT STRAND 80 82
 FT STRAND 85 90
 FT STRAND 97 98
 FT STRAND 102 106
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11902 MW; 9E8143E1188BCE2A CRC64;
 Query Match 9.2%; Score 10; DB 1; Length 108;
 Best Local Similarity 100.0%; Pred. No. 0.0025;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8
 KVSQ_MOUSE STANDARD; PRT; 108 AA.
 ID KVSQ_MOUSE
 DB 40 PGKAPKILLY 49
 QY 42 PGKAPKILLY 51
 |||||
 DB 40 PGKAPKILLY 49

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AC P01650;
AC 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region UPC 61.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79195288; PubMed=109517;
RA Vrana M., Rudikoff S., Potter M.;
RT "The structural basis of a hapten-inhibitable kappa-chain idiotype.";
RL J. Immunol. 122:1905-1910(1979).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT
CC BIND BETA(2-1)-FRUCTOFURANOSYL MOIETIES (INULIN).
DR HSSP; P80362; 1WTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 FRAMEWORK-4.
FT DOMAIN 98 108 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 88 FRAMEWORK-4.
FT NON TER 108 88 BY SIMILARITY.
SQ SEQUENCE 108 AA; 11809 MW; FAEADA36076F2AFB CRC64;

Query Match 9.2%; Score 10; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 PGKAPKLITY 51
DB 40 PGKAPKLITY 49

RESULT 9
KVSR MOUSE STANDARD; PRT; 108 AA.
ID KVSR MOUSE STANDARD; PRT; 108 AA.
AC P01651;
AC 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region EPC 109.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79195288; PubMed=109517;
RA Vrana M., Rudikoff S., Potter M.;
RT "The structural basis of a hapten-inhibitable kappa-chain idiotype.";
RL J. Immunol. 122:1905-1910(1979).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT
CC BIND BETA(2-1)-FRUCTOFURANOSYL MOIETIES (INULIN).
DR HSSP; P01607; 1RET.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.

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FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 FRAMEWORK-4.
FT DOMAIN 98 108 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 88 FRAMEWORK-4.
FT NON TER 108 88 BY SIMILARITY.
SQ SEQUENCE 108 AA; 11876 MW; 35CL16BD60F79310 CRC64;

Query Match 9.2%; Score 10; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 PGKAPKLITY 51
DB 40 PGKAPKLITY 49

RESULT 10
KVSR MOUSE STANDARD; PRT; 108 AA.
ID KVSR MOUSE STANDARD; PRT; 108 AA.
AC P01652;
AC 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region J606.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=82099361; PubMed=6798111;
RA Johnson N., Stankard J., Paul L.;
RT "The complete V domain amino acid sequences of two myeloma inulin-
RT binding proteins.";
RL J. Immunol. 128:302-307(1982).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT
CC BIND BETA(2-1)-FRUCTOFURANOSYL MOIETIES (INULIN).
DR HSSP; A92811; KVM506.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 FRAMEWORK-4.
FT DOMAIN 98 108 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 88 FRAMEWORK-4.
FT NON TER 108 88 BY SIMILARITY.
SQ SEQUENCE 108 AA; 11810 MW; 8DEADD31076F2AFB CRC64;

Query Match 9.2%; Score 10; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 PGKAPKLITY 51
DB 40 PGKAPKLITY 49

RESULT 11
KVSR MOUSE STANDARD; PRT; 108 AA.
ID KVSR MOUSE STANDARD; PRT; 108 AA.
AC P01653;

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DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG kappa chain V-V region W3082.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 NCBI_TaxID=10090;
 RX MEDLINE=82099361; PubMed=6798111;
 RA Johnson N., Slankard J., Paul L., Hood L.;
 RT "The complete V domain amino acid sequences of two myeloma inulin-
 binding proteins."
 RT J. Immunol. 128:302-307(1982).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT
 BIND BETA(2-1)-FRUCTOFURANOSYL MOIETIES (INULIN).
 DR PIR; B92811; KIMS82.
 DR HSSP; P80362; 1MTL.
 DR InterPro; IPR007110; IG_LIKE.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IGV_1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 2 34 FRAMEWORK-2.
 FT DOMAIN 3 49 FRAMEWORK-3.
 FT DOMAIN 4 56 FRAMEWORK-4.
 FT DOMAIN 5 57 FRAMEWORK-5.
 FT DOMAIN 6 88 FRAMEWORK-6.
 FT DOMAIN 7 97 FRAMEWORK-7.
 FT DOMAIN 8 108 FRAMEWORK-8.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON TER 108
 SQ SEQUENCE 108 AA; 11850 MW; C5C145DC376F30CD CRC64;
 Query Match 9.2%; Score 10; DB 1; Length 108;
 Best Local Similarity 100.0%; Pred. No. 0.0025;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 42 GKAPKLLITY 51
 DB 40 GKAPKLLITY 49
 RESULT 12
 LV3A HUMAN STANDARD; PRT; 108 AA.
 AC P01714;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE IG lambda chain V-II region SH.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RX MEDLINE=70166723; PubMed=4909564;
 RA Titani K., Wikler M., Shinoda T., Putnam F.W.;
 RT "The amino acid sequence of a lambda type Bence-Jones protein. 3. The
 complete amino acid sequence and the location of the disulfide
 bridges."
 RT J. Biol. Chem. 245:2171-2176(1970).
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A01980; L3H0SH.
 DR HSSP; P80748; 2LOI.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-LIKE.

DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IGV_1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DISULFID 21 86
 FT NON TER 108
 SQ SEQUENCE 108 AA; 11392 MW; E7E1229586411A56 CRC64;
 Query Match 9.2%; Score 10; DB 1; Length 108;
 Best Local Similarity 100.0%; Pred. No. 0.0025;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 81 QAEDEADYYC 90
 DB 77 QAEDEADYYC 86
 RESULT 13
 KVIS HUMAN STANDARD; PRT; 108 AA.
 ID LV3A HUMAN STANDARD; PRT; 108 AA.
 AC P01611;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG kappa chain V-I region Wes;
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RX MEDLINE=81092279; PubMed=6778806;
 RA Kratzin H., Yang C., Krusche J.U., Hilschmann N.;
 RT "Preparative separation of the tryptic hydrolysate of a protein by
 high-pressure liquid chromatography. The primary structure of a
 monoclonal L-chain of K-type, subgroup I (Bence-Jones protein
 Wes)."
 RT Hoppe-Seyler's Z. Physiol. Chem. 361:1591-1598(1980).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
 DR PIR; A01877; K1H0WS.
 DR HSSP; P80362; 1MTL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-LIKE.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IGV_1.
 DR SMART; SM00406; IGV_1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 2 34 FRAMEWORK-2.
 FT DOMAIN 3 49 FRAMEWORK-3.
 FT DOMAIN 4 56 FRAMEWORK-4.
 FT DOMAIN 5 57 FRAMEWORK-5.
 FT DOMAIN 6 88 FRAMEWORK-6.
 FT DOMAIN 7 97 FRAMEWORK-7.
 FT DOMAIN 8 107 FRAMEWORK-8.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON TER 108
 SQ SEQUENCE 108 AA; 11608 MW; 782B14A649A60B45 CRC64;
 Query Match 8.3%; Score 9; DB 1; Length 108;
 Best Local Similarity 100.0%; Pred. No. 0.025;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 43 GKAPKLLITY 51
 DB 41 GKAPKLLITY 49


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RESULT 14
KVIT_HUMAN
ID KVIIT_HUMAN STANDARD; PRT; 109 AA.
AC P01612;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig kappa chain V-I region Mew.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CX NCB1_TaxID=9606;
[1]
RN
RP MEDLINE=83081018; PubMed=6816713;
RA Eulitz M., Linke R.P.;
RT "Primary structure of the variable part of an amyloidogenic
RT Bence-Jones protein (Mew). An unusual insertion in the third
RT hypervariable region of a human kappa-immunoglobulin light chain.",
RL Hoppe-Seyler's Z. Physiol. Chem. 363:1347-1358(1982).
CC -1- MISCELLANEOUS; ANOTHER FORM THAT LACKED RESIDUES 1-3 WAS ALSO
CC FOUND.
CC -1- MISCELLANEOUS; THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
CC PIR; A01879; K1HMV.
DR HSSP; P80362; 1WTU.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 98 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 99 108 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 109 109
SQ SEQUENCE 109 AA; 11870 MW; B6BP4515D55FSA0 CRC64;

Query Match
Best Local Similarity 100.0%; Score 9; DB 1; Length 109;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 PGKAPKLT 50
DB 40 PGKAPKLT 48

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RESULT 15
KVIT_HUMAN
ID KVIIT_HUMAN STANDARD; PRT; 108 AA.
AC P01598;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region EU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CX NCB1_TaxID=9606;
[1]
RN
RP MEDLINE=71064023; PubMed=5489770;
RA Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino
RT acid sequence of the light chain.",
RL Biochemistry 9:3155-3161(1970).
CC -1- MISCELLANEOUS; THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
CC PIR; A03662; K1HEU.
DR HSSP; P01607; 1RET.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11788 MW; 9CD294F2FD88823 CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 1; Length 108;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 PGKAPKLT 49
DB 40 PGKAPKLT 47

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RESULT 16
KVIT_HUMAN
ID KVIIT_HUMAN STANDARD; PRT; 108 AA.
AC P01604;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Kue.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CX NCB1_TaxID=9606;
[1]
RN
RP MEDLINE=79237924; PubMed=112021;
RA Eulitz M., Kley H.-P., Zeitler H.-U.;
RT "The primary structure of the Bence-Jones protein Kue. The amino acid
RT sequence of the variable part of a human I-chain of the kappa-type.",
RL Hoppe-Seyler's Z. Physiol. Chem. 360:725-734(1979).
CC -1- MISCELLANEOUS; THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS; THIS IS A Bence-Jones protein.
CC PIR; A01870; K1HUKU.
DR HSSP; P01607; 1RET.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.

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FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 107 FRAMEWORK-4.
 FT DISULFID 23 86 BY SIMILARITY.
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 12127 MW; 906679A5D90E4E98 CRC64;

Query Match 7.3%; Score 8; DB 1; Length 108;
 Best Local Similarity 100.0%; Pred. No. 0.34;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 44 KAPPLITY 51
 Db 42 KAPPLITY 49

RESULT 17
 LVIF_HUMAN STANDARD; PRT; 109 AA.

AC P04208;
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 20-MAR-1987 (Rel. 04, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE 1g lambda chain V-I region MAH.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 CX NCBI_Taxid=9606;

RP SEQUENCE.
 RA MEDLINE=83221661; PubMed=6407018;
 RX Takahashi Y., Takahashi N., Teraert D., Putnam F.W.;
 RT "Complete covalent structure of a human immunoglobulin D: sequence of
 the lambda light chain.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:3686-3690(1983).
 DR HSSP; P01703; 7FAB.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; I9-like.
 DR Pfam; PF00047; I9; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; I9_LIKE; 1.

KW Immunoglobulin V region.
 FT DOMAIN 1 97 V SEGMENT.
 FT DOMAIN 98 109 J SEGMENT.
 FT DISULFID 22 89 BY SIMILARITY.
 FT NON TER 109 109
 SQ SEQUENCE 109 AA; 11725 MW; B17785F6A8DF9BAC CRC64;

Query Match 7.3%; Score 8; DB 1; Length 109;
 Best Local Similarity 100.0%; Pred. No. 0.34;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 63 RFGSKSG 70
 Db 62 RFGSKSG 69

RESULT 18
 LVII_HUMAN STANDARD; PRT; 109 AA.
 AC P06888;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE 1g lambda chain V-I region EPS.
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 CX NCBI_Taxid=9606;
 RP SEQUENCE.
 RX MEDLINE=86000126; PubMed=3929803;
 RA Toft K.G., Sletten K., Huseby G.;
 RT "The amino acid sequence of the variable region of a carbohydrate-
 containing amyloid fibril protein (immunoglobulin light chain,
 type lambda).";
 RL Biol. Chem. Hoppe-Seyler 366:617-625(1985).
 CC -I- MISCELLANEOUS: RESIDUES 1-2, 56-62, AND 74-78 AND THE SEQUENCED
 PEPTIDES WERE POSITIONED BY HOMOLOGY.
 CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.

DR PIR; A24656; LIHUP.
 DR HSSP; P01703; 7FAB.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; I9-like.
 DR Pfam; PF00047; I9; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; I9_LIKE; 1.
 KW Immunoglobulin V region; Amyloid; Glycoprotein.
 FT DOMAIN 1 105 I9-LIKE.
 FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .).
 FT DISULFID 22 89 BY SIMILARITY.
 FT NON TER 109 109
 SQ SEQUENCE 109 AA; 11414 MW; 556A313E24D5AC73 CRC64;

Query Match 7.3%; Score 8; DB 1; Length 109;
 Best Local Similarity 100.0%; Pred. No. 0.34;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 63 RFGSKSG 70
 Db 62 RFGSKSG 69

RESULT 19
 KVII_RABIT STANDARD; PRT; 94 AA.
 ID KVII_RABIT
 AC P01692;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE 1g kappa-B5 chain V region 2699 (Fragments).
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 CX NCBI_Taxid=9986;
 RP SEQUENCE.
 RX MEDLINE=83178897; PubMed=6404296;
 RA Ayadi H., Dutka S., Paroutaud P., Strosberg A.D.;
 RT "Partial amino acid sequence of a rabbit immunoglobulin light chain
 of allotype B5.";
 RL Biochemistry 22:993-998(1983).
 CC -I- MISCELLANEOUS: THIS CHAIN IS AN ANTIBODY TO PNEUMOCOCCUS STRAIN
 III VACCINE.

DR PIR; A01955; A01955.
 DR HSSP; P01607; IRLI.
 DR InterPro; IPR007110; I9-like.
 DR InterPro; IPR003599; I9.
 DR SMART; SM00409; IGV; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 82
 FT NON_CONS 82 83
 FRAMEWORK-1.
 COMPLEMENTARITY-DETERMINING-1.
 FRAMEWORK-2.
 COMPLEMENTARITY-DETERMINING-2.
 FRAMEWORK-3.

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FT DOMAIN <83 83 COMPLEMENTARITY-DETERMINING-3.
FT VARIANT 8 93 FRAMEWORK-4.
FT VARIANT 22 8 P -> A.
FT NON TER 22 22 N -> K.
SQ SEQUENCE 94 AA, 9469 MW, 35197783252EBC CRC64;

Query Match 6.4%; Score 7; DB 1; Length 94;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 100 FGGGKTV 106
Db 84 FGGGKTV 90

RESULT 20
LV4A_HUMAN STANDARD; PRT; 106 AA.
ID LV4A_HUMAN
AC P01715;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig lambda chain V-IV region Bau.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75059189; PubMed=4435717;
RA Baetzko K., Braun D., Hilschmann N.;
RT "Pattern of antibody structure, the primary structure of monoclonal
RT immunoglobulin L-chain of the lambda-type, subgroup IV (Bence-Jones
RT protein Bau).";
RL Hoppe-Seyler's Z. Physiol. Chem. 355:131-154(1974).
CC -1- SIMILARITY: This is a Bence-Jones protein.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSSP; P80748; 2LOI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 102
FT NON TER 106
SQ SEQUENCE 106 AA, 11305 MW, 4B6A6880EC46571 CRC64;

Query Match 6.4%; Score 7; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 84 DEADYYC 90
Db 80 DEADYYC 86

RESULT 21
LV4B_HUMAN STANDARD; PRT; 106 AA.
ID LV4B_HUMAN
AC P01716;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig lambda chain V-IV region X.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=63088380; PubMed=4883841;
RA Milstein C., Clegg J.B., Jarvis J.W.;
RT "Immunoglobulin lambda-chains. The complete amino acid sequence of a
RT Bence-Jones protein.";
RL Biochem. J. 110:631-652(1968).
CC -1- SIMILARITY: This is a Bence-Jones protein.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A01982; L4HUX.
DR HSSP; P80748; 2LOI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 102
FT NON TER 106
SQ SEQUENCE 106 AA, 11334 MW, 24D04344AA812855 CRC64;

Query Match 6.4%; Score 7; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 84 DEADYYC 90
Db 80 DEADYYC 86

RESULT 22
LV4E_HUMAN STANDARD; PRT; 106 AA.
ID LV4E_HUMAN
AC P06889;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig lambda chain V-IV region MOL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=87156515; PubMed=3103603;
RA Holm E., Sletten K., Husby G.;
RT "Structural studies of a carbohydrate-containing
RT immunoglobulin-lambda-light-chain amyloid-fibril protein (AL) of
RT variable subgroup IIT.";
RL Biochem. J. 239:545-551(1986).
CC -1- SIMILARITY: RESIDUES 29-30 AND 56-58 WERE POSITIONED BY
CC -1- SIMILARITY: RESIDUES 29-30 AND 56-58 WERE POSITIONED BY
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A26019; L4HML.
DR HSSP; P80748; 2LOI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Amyloid; Glycoprotein.
FT DOMAIN 1 103
FT DISULFID 21 86 BY SIMILARITY.
FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (PROBABLE).
FT NON TER 106
SQ SEQUENCE 106 AA, 11272 MW, D9BB77D4797D2123 CRC64;

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Query Match 6.4%; Score 7; DB 1; Length 106;
 Best Local Similarity 100.0%; Pred. No. 3.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 DEADYYC 90
 DB 80 DEADYYC 86

RESULT 23

KVIM HUMAN STANDARD; PRT; 108 AA.
 AC P01605;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region Lay.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE.
 RX MEDLINE=77038198; PubMed=824717;
 RA Capra J.D., Klapper D.G.;
 RT "Complete amino acid sequence of the variable domains of two human
 RT IGM anti-gamma globulins (Lay/Pom) with shared idiotypic
 RT specificities";
 RL Scand. J. Immunol. 5:677-684(1976).
 CC -I- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
 CC CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,
 CC WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
 CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
 CC GLOBULIN ACTIVITY.
 CC PIR: A01871; KIMULY.
 DR HSP: P01607; IREI.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003596; IG_v.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; IGV_1.
 DR PROSITE: PS50835; IG-LIKE; 1.
 KM Immunoglobulin V region.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 23 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 107 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11834 MW; 7399933954314344 CRC64;

Query Match 6.4%; Score 7; DB 1; Length 108;
 Best Local Similarity 100.0%; Pred. No. 4;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 APKLLIY 51
 DB 43 APKLLIY 49

RESULT 24

KVLY HUMAN STANDARD; PRT; 108 AA.
 AC P80362;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Ig kappa chain V-I region MAT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=95086080; PubMed=7993911;
 RA Huang D.-B., Chang C.-H., Ainsworth C., Bruegger A.T., Eulitz M.,
 RA Solomon A., Stevens F.J., Schiffer M.;
 RT "Comparison of crystal structures of two homologous immunoglobulin
 RT structural origin of altered domain interactions in immunoglobulin
 RT light-chain dimers";
 RL Biochemistry 33:14848-14857(1994).
 RN (2)

RP SEQUENCE OF 1-35.
 RX MEDLINE=81267384; PubMed=6167731;
 RA Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
 RA Popp R.A., Solomon A.;
 RT "Characterization and preliminary crystallographic data on the VL-
 RT related fragment of the human Ki Bence Jones protein wac.";
 RL J. Mol. Biol. 147:185-193(1981).
 CC -I- MISCELLANEOUS: This is a Bence-Jones protein.
 DR PDB: 1WTI; 01-NOV-94.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003596; IG_v.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; IGV_1.
 DR PROSITE: PS50835; IG-LIKE; 1.
 KM Immunoglobulin V region; Bence-Jones protein; 3D-structure.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 23 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 107 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11737 MW; D9D941B3F0FAE697 CRC64;

Query Match 6.4%; Score 7; DB 1; Length 108;
 Best Local Similarity 100.0%; Pred. No. 4;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 FGGTKV 106
 DB 98 FGGTKV 104

RESULT 25

LVSA_HUMAN
ID LVSA_HUMAN STANDARD; PRT; 108 AA.
AC P01719;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE IG lambda chain V-V region DEL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75112179; PubMed=4452363;
RA Eulitz M.;
RT "A new subgroup of human I-chains of the lambda-type. Primary
structure of Bence-Jones protein DEL."
RL Eur. J. Biochem. 50:49-69(1974).
CC -1- MISCELLANEOUS: THIS IS THE FIRST SEQUENCED V REGION OF LAMEDA
CHAIN SUBGROUP V.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A01985; LSHUDL.
DR HSSP; P80748; 2101.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
KM Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 97 IG-LIKE.
FT NON_TER 108
SQ SEQUENCE 108 AA; 11342 MW; B8E8ED9C09CE451 CRC64;

Query Match 6.4%; Score 7; DB 1; Length 108;
Best Local Similarity 100.0%; Pred.No.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 84 DEADYYC 90
Db 80 DEADYYC 86

Search completed: March 15, 2004, 07:42:33
Job time : 19 secs